

OW protein - protein search, using sw model  
 Run on: August 28, 2002, 16:30:18 ; Search time 51.58 Seconds  
 (without alignments)  
 99.058 Million cell updates/sec  
 Title: US-09-813-383-1  
 Perfect score: 260  
 Sequence: 1 HHPARTAHYGLPQKSHGRT.....VHEFKNIVTPRTPPSOGKG 46  
 Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5  
 Searched: 747574 seqs, 111073796 residues  
 Total number of hits satisfying chosen parameters: 747574  
 Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000  
 Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : A\_Geneseq\_032802.\*  
 1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.\*  
 2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.\*  
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 4: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.\*  
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 8: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.\*  
 9: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.\*  
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 18: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.\*  
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 21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.\*  
 22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	260	100.0	46	19	AAW72360
2	260	100.0	170	15	AAW48592
3	260	100.0	170	17	AAW95406
4	260	100.0	171	17	AAW97627
5	260	100.0	171	17	AAW99580
6	260	100.0	171	20	AAW27284
7	260	100.0	171	21	AAW19513
8	260	100.0	171	21	AAW69394
9	260	100.0	171	21	AAW44234
10	260	100.0	186	21	AAW57090
11	260	100.0	197	17	AAW00399

12	260	100.0	197	21	AAW95922	Human myelin bindi
13	260	100.0	203	17	AAW06107	Foetal myelin basi
14	260	100.0	203	17	AAW06108	Foetal myelin basi
15	260	100.0	373	17	AAW06103	MP4 chimera (MBP21
16	260	100.0	375	17	AAW06104	MP4 chimera (Delta
17	260	100.0	385	17	AAW06102	MP3 chimera (MBP21
18	260	100.0	492	17	AAW06105	MP3 chimera (MBP21
19	252	96.9	170	14	AAW35440	Human basic myelin
20	234	90.0	168	11	AAW04717	Empirically determ
21	234	90.0	168	11	AAW48594	Rabbit myelin basi
22	234	90.0	170	14	AAW30736	Human MBP. Synthe
23	221.5	85.2	169	15	AAW48593	Cattle myelin basi
24	220.5	84.8	170	11	AAW02226	Myelin basic prote
25	220.5	84.8	170	14	AAW30735	Bovine MBP. Synth
26	220.5	84.8	170	15	AAW45947	Myelin basic prote
27	220.5	84.8	170	17	AAW86422	Myelin basic prote
28	220.5	84.8	170	19	AAW57236	Myelin basic prote
29	220.5	84.8	170	21	AAW58368	Mammalian generic
30	220	84.6	41	20	AAW04044	Human myelin basic
31	201.5	77.5	167	15	AAW48595	Myelin basic prote
32	198	76.2	40	21	AAW12612	Human myelin basic
33	198	76.2	40	21	AAW85559	Human MBP peptide
34	197.5	76.0	127	15	AAW48596	Rat myelin basic p
35	194	74.6	39	21	AAW85561	Human MBP peptide
36	142.5	54.8	103	22	AAW02049	Synthetic human ta
37	142.5	54.8	273	22	AAW02052	Synthetic human mu
38	142.5	54.8	342	22	AAW02053	Synthetic human mu
39	139	53.5	25	17	AAW95342	MBP-2.5 (80-104)
40	139	53.5	25	18	AAW43948	Human myelin basic
41	135	51.9	24	15	AAW49336	Myelin basic prote
42	135	51.9	24	16	AAW74158	Antigenic peptide
43	135	51.9	24	19	AAW54719	Peptide from Myell
44	135	51.9	24	22	AAW06294	Human Leukocyte An
45	135	51.9	24	22	AAW84534	Human leukocyte an

ALIGNMENTS

RESULT 1  
 AAW72360  
 ID AAW72360 standard; peptide; 46 AA.  
 AC AAW72360;  
 DT 16-DEC-1998 (first entry)  
 DE Human myelin basic protein fragment.  
 KW Human; myelin basic protein; MBP; multiple sclerosis; anti-MBP; MS.  
 OS Homo sapiens.  
 PN WO9845327-Al.  
 PD 15-OCT-1998.  
 PF 03-APR-1998; 98WO-CA00290.  
 PR 04-APR-1997; 97CA-2201841.  
 PA (UYAL-) UNIV ALBERTA.  
 PI Catz I, Warren KG;  
 DR WPI; 1998-568336/48.  
 PT Peptide and its derivatives for treatment of multiple sclerosis - is  
 PT capable of neutralising or modulating production of anti-myelin  
 PS basic protein  
 PS Disclosure; Page 15; 75pp; English.

CC The present sequence represents a myelin basic protein (MBP) protein  
 CC fragment used to produce MBP peptides. MBP peptides are capable of  
 CC neutralising or modulating the production of anti-myelin basic protein.  
 CC The present invention also describes a method for treating multiple  
 CC sclerosis (MS). The method comprises administering to the patient an  
 CC MBP peptide of the formula: R1-val-His-Phe-Phe-Asn-Ile-R2 where R1,  
 CC R2 = H, OH, or an amino acid residue and a polypeptide residue,  
 CC provided that R1 and R2 are not both H or OH at the same time.  
 XX  
 SQ Sequence 46 AA;

Query Match 100.0%; Score 260; DB 19; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-27;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGSUPQKSHGRTQDENPVVHFFKNIVTPTPPSQGK 46  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 hhpatahygslpqkshgrtqdenpvvhffknivtrtpppsqqgk 46

RESULT 2  
 AAR48592  
 ID AAR48592 standard; protein; 170 AA.  
 XX  
 AC AAR48592;  
 XX  
 DT 31-JUL-1994 (first entry)  
 XX  
 DE Human myelin basic protein.  
 XX  
 KW Proteolipid protein; myelin basic protein; retrovirus;  
 KW neurological disease; by-stander antigen; TGF-beta;  
 KW transforming growth factor-beta; T-cell; T-lymphocyte;  
 KW myelopathy; paraparesis; human immunodeficiency virus type 1.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9404121-A.  
 XX  
 PD 03-MAR-1994.  
 XX  
 PF 17-AUG-1993; 93WO-US07786.  
 XX  
 PR 17-AUG-1992; 92US-0931217.  
 XX  
 XX (AUTO-) AUTOIMMUNE INC.  
 PA  
 PI Hafler DA, Weiner HL;  
 XX  
 DR WPI; 1994-082786/10.  
 XX  
 PT Treating retroviral associated neurological disease - by admin.  
 PT of by-stander antigen, causing release of transforming growth  
 PT factor beta from suppressor T cells  
 XX  
 PS Disclosure; Page 49; 64pp; English.  
 XX

XX Myelin basic proteins (sequences AAR48592-96) and cattle proteolipid  
 CC protein (AAR48592) elicit the release of TGF-beta from suppressor T-  
 CC cells and target the T-cells to neural tissue under cytotoxic  
 CC attack, thereby reducing neurological disease, e.g. HTLV-1  
 CC associated myelopathy, tropical spastic paraparesis and HIV  
 CC infection.  
 XX  
 SQ Sequence 170 AA;

Query Match 100.0%; Score 260; DB 15; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGSUPQKSHGRTQDENPVVHFFKNIVTPTPPSQGK 46

Db 61 hhpatahygslpqkshgrtqdenpvvhffknivtrtpppsqqgk 106  
 ||||||||||||||||||||||||||||||||||||||||||||

RESULT 3  
 AAR95406  
 ID AAR95406 standard; Protein; 170 AA.  
 XX  
 AC AAR95406;  
 XX  
 DT 16-DEC-1996 (first entry)  
 XX  
 DE Myelin oligodendrocyte protein.

XX  
 KW Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE;  
 KW CD4+; autoimmune disease; demyelination; central nervous system;  
 KW CNS; animal model; human; multiple sclerosis; MS; mammal; benign MS; MOG;  
 KW relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PLP;  
 KW diabetes; Graves disease; myasthenia gravis; Good Pasture's syndrome;  
 KW psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG;  
 KW myelin oligodendrocyte protein; myelin associated glycoprotein; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9612737-A2.  
 XX  
 PD 02-MAY-1996.  
 XX  
 PF 25-OCT-1995; 95WO-US13682.  
 XX  
 PR 15-MAR-1995; 95US-0404228.  
 PR 25-OCT-1994; 94US-0328224.  
 PR 25-OCT-1995; 95ZA-0009033.  
 XX  
 XX (IMMU-) IMMULOGIC PHARM CORP.  
 PA  
 PI Devaux B, Franzen H, Geftner M, Hsu D, Paliard X;  
 PI Rothbard J, Samson M, Shi J, Smillek D;  
 XX  
 WPI; 1996-230552/23.

XX  
 PT Myelin basic derived peptide(s) and analogs - used in the treatment  
 PT of Multiple Sclerosis, psoriasis, Graves Disease, etc.  
 XX  
 PS Example 9; Fig 1; 91pp; English.

XX  
 CC This sequence represents the human myelin oligodendrocyte protein (MOG).  
 CC Immunisation with MOG (or the peptide fragments shown in  
 CC AAR95375-R95385) can be used to induce experimental allergic  
 CC encephalomyelitis (EAE) in susceptible strains of mice. EAE is a CD4+  
 CC T-cell mediated autoimmune disease which results in demyelination of the  
 CC central nervous system, resulting in paralysis and other neurological  
 CC abnormalities. EAE is a commonly used animal model for human multiple  
 CC sclerosis (MS). These sequences can be used in compositions for treating  
 CC MS in a mammal. The composition acts to down regulate the autoimmune  
 CC response, and may be administered in an amount sufficient to prevent the  
 CC onset of symptoms of MS. The compositions may also be used to treat  
 CC advanced stage MS. These peptides may also be used in the treatment of  
 CC MS or benign MS. These peptides may also be used in the treatment of  
 CC other diseases involving myelin autoantigens, including diabetes, Graves  
 CC disease, myasthenia gravis, Good Pasture's syndrome, psoriasis,  
 CC thyroiditis, and rheumatoid arthritis. Peptides derived from other  
 CC myelin autoantigens, such as myelin basic protein (MBP), see  
 CC AAR95334-R95374), proteolipid protein (PLP), and myelin associated  
 CC glycoprotein (MAG) can be used as alternatives to the MOG peptides in  
 CC these compositions.

XX  
 SQ Sequence 170 AA;

Query Match 100.0%; Score 260; DB 17; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGKG 46  
 |||||  
 Db 61 hhpatahygslpdkshgrtqdenpvvhffknivtrtpptpsqgkg 106

RESULT 4  
 AAR97627 standard; Protein; 171 AA.  
 XX  
 AC AAR97627;  
 XX  
 DT 09-NOV-1996 (first entry)  
 XX  
 DE Human myelin basic protein.  
 XX  
 KW Myelin basic protein; MBP; multiple sclerosis; MS; treatment;  
 KW prevention; analogue.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT Peptide  
 FT /label= Claimed peptide region.  
 XX  
 PN WO9616085-A1.

XX 30-MAY-1996.  
 XX  
 PF 16-NOV-1995; 95WO-US14402.  
 XX  
 PR 18-NOV-1994; 94US-0342078.  
 XX  
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 XX (STRD ) UNIV STANFORD MEDICAL CENT.  
 XX  
 PI Conlon PJ, Gaur A, Ling N, Steinman L;  
 XX  
 DR WPI; 1996-268534/27.  
 DR N-PSDB; AAT30269.  
 XX  
 PT Peptide analogue of human myelin basic protein - has Lysine 91  
 PT replaced by another amino acid, useful to treat multiple sclerosis  
 XX  
 PS Claim 1; Figure 1; 30pp; English.  
 XX  
 CC A peptide analogue comprising amino acids 87-99 of human myelin  
 CC basic protein (MBP), where Lys91 is substituted for another amino  
 CC acid can be used to treat and prevent multiple sclerosis. The  
 CC peptide analogue is administered at a dosage range of 5-50 mg/kg.  
 XX  
 SQ Sequence 171 AA;

Query Match 100.0%; Score 260; DB 17; Length 171;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGKG 46  
 |||||  
 Db 62 hhpatahygslpdkshgrtqdenpvvhffknivtrtpptpsqgkg 107

RESULT 5  
 AAR99580 standard; Protein; 171 AA.  
 XX  
 AC AAR99580;  
 XX  
 DT 07-NOV-1996 (first entry)  
 XX  
 DE Human myelin basic protein (MBP).  
 XX

KW Myelin basic protein; MBP; multiple sclerosis; MS; competition;  
 KW inhibition; major histocompatibility complex; MHC; thymocyte; T cell;  
 XX experimental allergic encephalomyelitis; EAE; analogue.  
 OS Homo sapiens.

XX WO9616086-A1.  
 XX 30-MAY-1996.  
 XX  
 PF 16-NOV-1995; 95WO-US14403.  
 XX  
 PR 18-NOV-1994; 94US-0342408.  
 XX  
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 XX  
 PI Conlon PJ, Gaur A, Ling N, Steinman L;  
 XX  
 DR WPI; 1996-268535/27.  
 DR N-PSDB; AAT32561.

XX Peptide analogues of human myelin basic protein - useful for  
 PT treatment of multiple sclerosis  
 XX  
 PS Disclosure; Figure 1; 61pp; English.  
 XX

XX Peptide analogues comprising at least seven amino acids from  
 CC residues 86-99 of human myelin basic protein (MBP), can be used to  
 CC treat multiple sclerosis by competing for the binding of native MBP  
 CC peptide to MHC and by not causing proliferation of an MBP reactive T-  
 CC cell line. The peptide analogues also inhibit the induction of  
 CC experimental allergic encephalomyelitis (EAE) by MBP in rodents.  
 CC The peptide analogues have a reduced susceptibility to proteolysis  
 CC in vivo.

XX SQ Sequence 171 AA;

Query Match 100.0%; Score 260; DB 17; Length 171;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGKG 46  
 |||||  
 Db 62 hhpatahygslpdkshgrtqdenpvvhffknivtrtpptpsqgkg 107

RESULT 6  
 AAY27284 standard; Protein; 171 AA.  
 XX  
 AC AAY27284;  
 XX

DT 29-OCT-1999 (first entry)

DE Human myelin basic protein (MBP).

XX Myelin basic protein; MBP; peptide analogue; MHC; multiple sclerosis;  
 KW T-cell reactivity; major histocompatibility complex; human.  
 XX

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 86..99  
 FT /note= "peptide analogues of the invention comprise  
 FT at least seven consecutive amino acid residues  
 FT from this region"

FT Misc-difference 97

FT /note= "the L-Arg at this position can be altered to  
 FT a D-amino acid and especially to a D-Ala to  
 FT construct the peptide analogues (see claims 2  
 FT and 3"

PN US5948764-A.  
 XX  
 PD 07-SEP-1999.  
 XX  
 PF 09-JAN-1997; 97US-0781122.  
 XX  
 PR 09-JAN-1997; 97US-0781122.  
 PR 09-MAR-1995; 95US-0402992.  
 XX  
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 XX  
 PI Conlon PJ, Gaur A, Ling N;  
 XX WPI: 1999-517966/43.  
 DR N-PSDB; AA200399.  
 XX  
 PT Human myelin basic protein analogues useful for the treatment of  
 PT multiple sclerosis  
 PS  
 PS Disclosure; Fig 1; 35pp; English.  
 XX  
 CC The invention provides human myelin basic protein (MBP) analogues. The  
 CC analogues, comprise a sequence of 7 or more consecutive amino acids  
 CC taken from between residues 86 to 99 of the native human MBP amino acid  
 CC sequence (AA27284). The analogues include residue 97 of the human MBP  
 CC sequence, however, the L-arginine at position 97 is altered to a D-amino  
 CC acid. The peptide analogues may be used for treating multiple sclerosis.  
 CC Multiple sclerosis may be caused by an autoimmune reaction involving  
 CC T-cells which have lost their 'self-tolerance' and attack normal tissue.  
 CC Therefore, T-cell reactivity to human MBP may be a major cause of the  
 CC development of MS. The T-cells recognize and bind to an epitope of human  
 CC MBP between amino acids 86 to 106 of the sequence. The peptide analogues  
 CC have a higher binding affinity for major histocompatibility complexes  
 CC (MHC) on the T-cells than human MBP and therefore interfere with the  
 CC reactivity of T-cells against human MBP. Administration of the analogues  
 CC may prevent future, repeated attacks of multiple sclerosis without any  
 CC side effects after long-term use (such as malignancies, toxic hepatitis  
 CC and immunocompromising the patient). The present sequence represents a  
 CC human MBP sequence.  
 XX  
 SQ Sequence 171 AA;  
 Query Match 100.0%; Score 260; DB 20; Length 171;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFKNIVTPTPPSQGKG 46  
 Db 62 hhpatahyglpdkshgrtqdenpvvhffknivtprtppsqqkg 107  
 RESULT 7  
 AAB19513  
 ID AAB19513 standard; Protein; 171 AA.  
 XX  
 AC AAB19513;  
 XX  
 DT 09-JAN-2001 (first entry)  
 XX  
 DE Human myelin basic protein.  
 XX  
 KW Myelin basic protein; human; autoimmune disease; autoantigen;  
 KW demyelinating disease; experimental autoimmune encephalitis;  
 KW multiple sclerosis; antiinflammatory; DNA vaccination; vaccine;  
 KW T cell; pro-inflammatory response.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2000053019-A1.  
 XX  
 PD 14-SEP-2000.  
 XX  
 PF 09-JAN-1997; 97US-0781122.  
 PR 09-MAR-1995; 95US-0402992.  
 XX  
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 XX  
 PI Conlon PJ, Gaur A, Ling N;  
 XX WPI: 1999-517966/43.  
 DR N-PSDB; AA200399.  
 XX  
 PT Human myelin basic protein analogues useful for the treatment of  
 PT multiple sclerosis  
 PS  
 PS Disclosure; Fig 1; 35pp; English.  
 XX  
 CC The invention provides human myelin basic protein (MBP) analogues. The  
 CC analogues, comprise a sequence of 7 or more consecutive amino acids  
 CC taken from between residues 86 to 99 of the native human MBP amino acid  
 CC sequence (AA27284). The analogues include residue 97 of the human MBP  
 CC sequence, however, the L-arginine at position 97 is altered to a D-amino  
 CC acid. The peptide analogues may be used for treating multiple sclerosis.  
 CC Multiple sclerosis may be caused by an autoimmune reaction involving  
 CC T-cells which have lost their 'self-tolerance' and attack normal tissue.  
 CC Therefore, T-cell reactivity to human MBP may be a major cause of the  
 CC development of MS. The T-cells recognize and bind to an epitope of human  
 CC MBP between amino acids 86 to 106 of the sequence. The peptide analogues  
 CC have a higher binding affinity for major histocompatibility complexes  
 CC (MHC) on the T-cells than human MBP and therefore interfere with the  
 CC reactivity of T-cells against human MBP. Administration of the analogues  
 CC may prevent future, repeated attacks of multiple sclerosis without any  
 CC side effects after long-term use (such as malignancies, toxic hepatitis  
 CC and immunocompromising the patient). The present sequence represents a  
 CC human MBP sequence.  
 XX  
 SQ Sequence 171 AA;  
 Query Match 100.0%; Score 260; DB 20; Length 171;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFKNIVTPTPPSQGKG 46  
 Db 62 hhpatahyglpdkshgrtqdenpvvhffknivtprtppsqqkg 107  
 RESULT 8  
 AAY69394  
 ID AAY69394 standard; Protein; 171 AA.  
 XX  
 AC AAY69394;  
 XX  
 DT 19-JUN-2000 (first entry)  
 XX  
 DE Amino acid sequence of a human myelin basic protein.  
 XX  
 KW Human; myelin basic protein; oligodendroglial cell; Th2 immune response;  
 KW Th2-type cytokine; analogue; multiple sclerosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200011027-A1.  
 XX  
 PD 02-MAR-2000.  
 XX  
 PF 19-AUG-1999; 99WO-US19033.  
 PR 20-AUG-1998; 98US-0137759.  
 XX  
 PA (NOVS ) NOVARTIS AG.  
 PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 XX

PI Gaur A, Conlon P, Ling NC, Staehlin T, Crowe P;  
 XX WPI: 2000-224661/19.  
 DR N-PSDB; AAZ61594.  
 XX Inducing a Th2 immune response and a persistent systemic immune  
 PT response to myelin basic protein, MBP, or a peptide analog of MBP for  
 FT use in treating multiple sclerosis, by administering compositions  
 PT comprising peptide analogs of MBP -  
 XX  
 XX Disclosure: Fig 1; 112pp; English.  
 XX The present sequence represents a human myelin basic protein. Myelin  
 CC basic protein is found in the cytoplasm of human oligodendroglial  
 CC cells. Peptide analogues of myelin basic protein are administered to  
 CC a patient in need to induce a Th2 immune response (i.e. production  
 CC of T cells producing one or more Th2-type cytokines) and/or a  
 CC persistent systemic immune response to myelin basic protein. These  
 CC peptide analogues are at least seven amino acids long, derived from  
 CC residues 83-99 of human myelin basic protein and altered from the  
 CC native sequence at least at positions 91, 95 or 97. The peptide  
 CC analogs are especially useful in the treatment of multiple sclerosis.  
 XX  
 XX Sequence 171 AA;

Query Match 100.0%; Score 260; DB 21; Length 171;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLPQKSHGRQDENPVVHFFKNIPTPTPPSQGK 46  
 DB 62 hhpatahygslpckshgrtqdenpvvhffkniptptppsqgk 107

RESULT 9

AAAY44234  
 ID AAY44234 standard; Protein; 171 AA.

AC AAY44234;

DT 21-FEB-2000 (first entry)

DE Human myelin basic protein.

XX Human; myelin basic protein; MBP; NS-specific antigen;  
 KW nervous system-specific antigen; T cell; peripheral nervous system; PNS;  
 KW central nervous system; CNS; nerve regeneration; neuronal degeneration;  
 KW spinal cord injury; blunt trauma; penetrating trauma; senile dementia;  
 KW ischaemic stroke; diabetic neuropathy; glaucoma; haemorrhagic stroke;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's chorea;  
 KW amyotrophic lateral sclerosis; ALS; treatment.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 11..30

FT /label= Cryptic epitope  
 FT /note= "activates T cells by itself but does not  
 FT induce an autoimmune disease"

FT Peptide 51..70

FT /label= Cryptic epitope  
 FT /note= "activates T cells by itself but does not  
 FT induce an autoimmune disease"

FT Peptide 91..110

FT /label= Cryptic epitope  
 FT /note= "activates T cells by itself but does not  
 FT induce an autoimmune disease"

FT Peptide 131..150

FT /label= Cryptic epitope  
 FT /note= "activates T cells by itself but does not  
 FT induce an autoimmune disease"

FT Peptide 151..170

FT /label= Cryptic epitope  
 FT /note= "activates T cells by itself but does not  
 FT induce an autoimmune disease"  
 XX WO9960021-A2.  
 XX 25-NOV-1999.  
 XX 19-MAY-1999; 99WO-US10953.  
 XX 19-MAY-1998; 98IL-0124550.  
 XX 21-JUL-1998; 98WO-US14715.  
 XX 22-DEC-1998; 98US-0218277.  
 XX (YEDA ) YEDA RES & DEV CO LTD.  
 XX (MCIN/) MCINNIS P A.  
 XX Eisenbach-Schwartz M, Cohen IR, Beserman P, Mosonogo A, Moalem G;  
 PI WPI: 2000-072430/06.  
 DR N-PSDB; AAZ29197.  
 XX New compositions useful to treat nervous system injury or disease e.g.  
 PT traumatic injury, Alzheimer's disease etc.  
 XX Claim 9; Fig 21; 92pp; English.

XX The present sequence is a human myelin basic protein  
 CC which is a nervous system-specific antigen. The antigen or peptides  
 CC derived from it activate T cells in vivo. The present sequence is  
 CC used to promote nerve regeneration or to prevent or inhibit neuronal  
 CC degeneration caused by injury or diseases of nerves within the CNS or  
 CC PNS. Such injury includes spinal cord injury, blunt trauma, penetrating  
 CC trauma, haemorrhagic stroke or ischaemic stroke, whilst diseases include  
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's  
 CC disease, glaucoma, Huntington's chorea, amyotrophic lateral sclerosis,  
 CC etc.

XX Sequence 171 AA;

Query Match 100.0%; Score 260; DB 21; Length 171;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLPQKSHGRQDENPVVHFFKNIPTPTPPSQGK 46  
 DB 62 hhpatahygslpckshgrtqdenpvvhffkniptptppsqgk 107

RESULT 10

AAAY57090

ID AAY57090 standard; protein; 186 AA.

XX AAY57090;

XX 28-FEB-2000 (first entry)

XX Human myelin basic protein fragment.

XX Neglected target tissue antigen; NNTA; autoimmunity; autoimmune response;  
 KW immunotherapeutic agent; insulin dependent diabetes mellitus;  
 KW multiple sclerosis; autoimmune thyroiditis; rheumatoid arthritis;  
 KW uveoretinitis; inflammatory response.

XX Homo sapiens.

XX WO9956763-A1.

XX 11-NOV-1999.

XX 07-MAY-1999; 99WO-US10250.

PR 07-MAY-1998; 98US-0084636.  
 XX (REGC ) UNIV CALIFORNIA.  
 PA Kaufman DL, Tian J, Olcott A;  
 PI WPI; 2000-052905/04.  
 XX  
 XX Administration of neglected target tissue antigens to modulate immune  
 PT responses  
 XX  
 XX Disclosure; Page 33; 79pp; English.  
 PS  
 XX Amino acid sequences AAY57063-Y57091 are examples of neglected target  
 CC tissue antigens NRTAs. NRTAs are antigens (whole antigens or fragments)  
 CC not involved in autoimmunity. These peptides and proteins are used in  
 CC the method of the invention which involves administering an NRTA as an  
 CC antigen based immunotherapeutic agent, to a host afflicted with an  
 CC autoimmune response associated with an autoimmune disease. The  
 CC immunotherapeutic agent is used to treat autoimmune diseases such as  
 CC insulin dependent diabetes mellitus, multiple sclerosis, autoimmune  
 CC thyroiditis, uveoretinitis, rheumatoid arthritis or abnormal  
 CC inflammatory immune responses. The NRTA induces regulatory tolerance by  
 CC elicitation of regulatory T cells among T cells recognizing the NRTA but  
 CC not participating in the immune response. The NRTA are capable of  
 CC recognition by substantial populations of uncommitted T cells which can  
 CC be primed, or biased, towards regulatory responses to provide effective  
 CC treatment. The NRTA are effective in regulating undesirable immune  
 CC responses even when target determinants used as agents promoting  
 CC tolerance agents have failed to induce an effective regulatory T cell  
 CC response. NRTAs as agents promoting tolerance are anticipated to be safer  
 CC than use of target determinants.  
 XX  
 XX Sequence 186 AA;  
 SQ

Query Match 100.0%; Score 260; DB 21; Length 186;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-26;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPPPSQGGK 46  
 DB 88 hhpatahygslpqkshgrtqdenpvvhffknivtprtpppsqgk 133

RESULT 11  
 AAW00399  
 ID AAW00399 standard; Protein; 197 AA.  
 XX  
 AC AAW00399;  
 XX  
 DT 01-FEB-1997 (first entry)  
 XX  
 XX Human myelin basic protein (foetal isoform).  
 XX  
 XX Myelin basic protein; MBP; MBP+X2Cys81; proteolipid protein; PLP;  
 KW multiple sclerosis; autoimmune disease; diagnosis; therapy;  
 KW T-lymphocyte; T-cell; anergy; apoptosis.  
 XX  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH Region 60..85  
 FT /label= X2  
 FT /note= "exon 2-encoded region"  
 FT Misc-difference 81  
 FT /note= "Cys-81 may be replaced by any standard  
 FT amino acid, esp. an uncharged amino acid  
 FT of mol.wt. below about 150, partic.  
 FT Ser, in constructs of the invention"  
 XX  
 XX WO9634622-A1.  
 PN  
 XX

PD 07-NOV-1996.  
 XX  
 PF 22-APR-1996; 96WO-US05611.  
 XX  
 PR 07-JUN-1995; 95US-0482114.  
 PR 02-MAY-1995; 95US-0431644.  
 PR 02-MAY-1995; 95US-0431648.  
 XX  
 XX (ALEX-) ALEXION PHARM INC.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Lenardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;  
 PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;  
 XX  
 DR WPI; 1996-505898/50.  
 DR N-PSDB; AAT41889.  
 XX  
 XX New human myelin basic protein and proteolipid protein variant(s) -  
 PT used in the assessment, diagnosis and treatment of multiple  
 PT sclerosis  
 XX  
 PS Claim 1; Page 79-80; 156pp; English.  
 XX  
 CC The native human 21.5 kDa foetal isoform (AAW00399) of myelin basic  
 CC protein, MBP+X2Cys81, includes an exon 2-encoded region (X2) that  
 CC may contain an epitope involved in the pathogenesis of multiple  
 CC sclerosis (MS); the X2 region is not found in the MBP of healthy  
 CC adults. Recombinant MBP+X2 or variants modified to improve  
 CC bacterial expression (see also AAW06107), can be produced in a  
 CC large scale in bacterial hosts. They are useful for assaying  
 CC T-cells for responsiveness to MBP epitopes and can be used as  
 CC therapeutic agents that act by inducing T-cell responses,  
 CC including anergy and apoptosis, as a means of treating MS.  
 XX  
 XX Sequence 197 AA;  
 SQ

Query Match 100.0%; Score 260; DB 17; Length 197;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-26;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPPPSQGGK 46  
 DB 88 hhpatahygslpqkshgrtqdenpvvhffknivtprtpppsqgk 133

RESULT 12  
 AAY95922  
 ID AAY95922 standard; Protein; 197 AA.  
 XX  
 AC AAY95922;  
 XX  
 DT 20-NOV-2000 (first entry)  
 XX  
 XX Human myelin binding protein Delta II.  
 XX  
 XX Myelin binding protein; MBP; human; GPBP;  
 KW goodpasture antigen binding protein; autoimmune disease; apoptosis;  
 KW cancer; tumour; therapy.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200050607-A2.  
 PN  
 XX 31-AUG-2000.  
 PD  
 XX 24-FEB-2000; 2000WO-IB00324.  
 PF  
 XX 24-FEB-1999; 99US-0121483.  
 PR  
 XX (SAUS/) SAUS J.  
 PA  
 XX Saus J;  
 PI

XX WPI: 2000-572094/53.  
 DR N-PSDB; AAA50371.  
 XX  
 PT Novel Goodpasture antigen binding proteins useful for diagnosing and  
 PS treating autoimmune disorders, tumor, and preventing cell apoptosis -  
 XX  
 PS Claim 36; Page 157; 158pp; English.  
 XX  
 CC The present sequence is that of human myelin binding protein (MBP)  
 CC Delta II, i.e. an alternative form of human MBP resulting from  
 CC splicing out of exon II. The protein was recombinantly expressed in  
 CC Pichia pastoris cells. The invention relates to novel Goodpasture  
 CC antigen binding proteins (GPBs), see AAY95900-11), which bind to and  
 CC phosphorylate the unique N-terminal region of human GP, and which  
 CC are highly expressed in several autoimmune conditions. Claimed  
 CC methods for treating an autoimmune disorder, cell apoptosis or a  
 CC tumour involve modifying the expression or activity of GPBP,  
 CC especially using a MBP protein or a nucleic acid sequence encoding  
 CC it.  
 XX Sequence 197 AA;  
 SQ

Query Match 100.0%; Score 260; DB 21; Length 197;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-26;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGSIPKSGHRTQDENPVVHFFKNIIVTPTPPSQGKG 46  
 Db 88 hhpatahygsipqksngrtcqdenpvvhffknivtprtppsqgkg 133

RESULT 13  
 AAW06107  
 ID AAW06107 standard; Protein; 203 AA.  
 XX  
 AC AAW06107;  
 XX

DT 01-FEB-1997 (first entry)  
 XX

DE Foetal myelin basic protein MBP+X2Cys81/bact.  
 XX

KW Myelin basic protein; MBP; MBP+X2Cys81; proteolipid protein; PLP;  
 KW multiple sclerosis; autoimmune disease; diagnosis; therapy;  
 KW T-lymphocyte; T-cell; anergy; apoptosis.  
 XX

OS Synthetic.  
 XX

FH Key Location/Qualifiers  
 FT Region 60..85  
 FT /label= X2  
 FT /note= "exon 2-encoded region"  
 XX

PN WO9634622-A1.  
 XX

PD 07-NOV-1996.  
 XX

PF 22-APR-1996; 96WO-US05611.  
 XX

PR 07-JUN-1995; 95US-0482114.  
 PR 02-MAY-1995; 95US-0431644.  
 PR 02-MAY-1995; 95US-0431648.  
 XX

PA (ALEX-) ALEXION PHARM INC.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX

PI Lenardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;  
 PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;  
 XX

DR WPI: 1996-505898/50.  
 DR N-PSDB; AAT41896.  
 XX

PT New human myelin basic protein and proteolipid protein variant(s) -  
 PT used in the assessment, diagnosis and treatment of multiple  
 PT sclerosis  
 XX  
 PS Disclosure; Page 81-82; 156pp; English.  
 XX  
 CC A 21.5 kDa foetal isoform (AAW06107) of myelin basic protein,  
 CC MBP+X2Cys81/bact., is the product of a DNA construct (AAT41896)  
 CC based on the human foetal MBP+X2Cys81 isoform (AAW00399) but  
 CC utilising bacterially-preferred codons in place of the native human  
 CC codons (see also AAT41899). This increases prodn. of the MBP in E.  
 CC coli by at least 50%. Recombinant MBP 21.5 polypeptides (see also  
 CC AAW00399 and AAW06108) are useful in the clinical assessment, diagnosis  
 CC and treatment of MS.  
 XX Sequence 203 AA;  
 SQ

Query Match 100.0%; Score 260; DB 17; Length 203;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-26;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGSIPKSGHRTQDENPVVHFFKNIIVTPTPPSQGKG 46  
 Db 88 hhpatahygsipqksngrtcqdenpvvhffknivtprtppsqgkg 133

RESULT 14  
 AAW06108  
 ID AAW06108 standard; Protein; 203 AA.  
 XX  
 AC AAW06108;  
 XX

DT 01-FEB-1997 (first entry)  
 XX

DE Foetal myelin basic protein MBP+X2Ser81/bact.  
 XX

KW Myelin basic protein; MBP; MBP+X2Ser81; proteolipid protein; PLP;  
 KW multiple sclerosis; autoimmune disease; diagnosis; therapy;  
 KW T-lymphocyte; T-cell; anergy; apoptosis.  
 XX

OS Synthetic.  
 XX

FH Key Location/Qualifiers  
 FT Region 60..85  
 FT /label= X2  
 FT /note= "exon 2-encoded region, with Cys81Ser  
 FT mutation"  
 XX

PN Peptide 198..203  
 XX

FT /label= Hexa-histidine tag  
 FT /note= "the hexa-histidine tag facilitates  
 FT purification of the recombinant protein  
 FT from host cells"  
 XX

PN WO9634622-A1.  
 XX

PD 07-NOV-1996.  
 XX

PF 22-APR-1996; 96WO-US05611.  
 XX

PR 07-JUN-1995; 95US-0482114.  
 PR 02-MAY-1995; 95US-0431644.  
 PR 02-MAY-1995; 95US-0431648.  
 XX

PA (ALEX-) ALEXION PHARM INC.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX

PI Lenardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;  
 PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;  
 XX

DR WPI: 1996-505898/50.  
 DR N-PSDB; AAT41897.  
 XX





XX MP4 chimera (AAW06103) is a fusion protein composed of human myelin  
 CC basic protein (MBP) foetal isoform MBP21.5 (see also AAW00399) and  
 CC delta PLP4 (AAW06101), a proteolipid protein (PLP) mutein that lacks  
 CC all 4 hydrophobic domains of native human PLP (AAW06106) but  
 CC includes PLP epitopes associated with multiple sclerosis (MS). It  
 CC can be expressed in E. coli transformants using a DNA construct  
 CC (ANT41893) contg. the MBP21.5-delta PLP4 gene fusion. MP4 chimera  
 CC and other novel PLP/MBP21.5 polypeptides (AAW00399-400, AAW06101-08)  
 CC are useful for the clinical assessment, diagnosis and treatment  
 CC of MS.  
 XX

SQ Sequence 373 AA;

Query Match 100.0%; Score 260; DB 17; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-26;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQKG 46  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Db 88 hhpatahygslpqlkshgrtqdenpvvhffknivtprtpppsqkg 133

Search completed: August 28, 2002, 16:35:03  
 Job time: 285 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 28, 2002, 16:32:18 ; Search time 20.54 Seconds  
(without alignments)  
54.702 Million cell updates/sec

Title: US-09-813-383-1

Perfect score: 260

Sequence: 1 HHPARTAHYGLPKSHGRT.....VHFFKNIVTPRTPPSQKG 46

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCRUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	260	100.0	170	2	US-08-327-357A-1
2	260	100.0	170	3	US-09-007-520-1
3	260	100.0	170	4	US-09-055-263-1
4	260	100.0	170	4	US-09-007-520-1
5	260	100.0	170	4	US-08-342-408B-2
6	260	100.0	171	2	US-08-781-122-2
7	260	100.0	171	4	US-09-137-759-2
8	234	90.0	168	6	5194425-4
9	220.5	84.8	170	1	US-08-227-372-1
10	220.5	84.8	170	3	US-08-462-351-3
11	220.5	84.8	170	6	5194425-3
12	219.5	84.4	170	3	US-08-470-397-1
13	198	76.2	40	3	US-08-297-395-2
14	195.5	75.2	170	6	5468481-3
15	135	51.9	24	2	US-08-480-190-46
16	135	51.9	24	2	US-08-488-379-46
17	135	51.9	24	5	PCT-US93-07545-46
18	128	49.2	23	1	US-08-787-547-1
19	128	49.2	24	1	US-08-305-871A-2
20	115	44.2	20	3	US-08-297-395-20
21	112	43.1	20	2	US-08-640-344-6
22	110	42.3	20	1	US-08-787-547-35
23	110	42.3	20	3	US-08-297-395-21
24	108	41.5	20	2	US-08-640-344-4
25	107	41.2	19	2	US-08-640-344-2
26	107	41.2	19	2	US-08-468-540B-9
27	107	41.2	19	3	US-08-297-395-1

28 107 41.2 19 4 US-09-024-220-2 Sequence 2, Appli  
29 107 41.2 19 4 US-08-960-190A-32 Sequence 32, Appli  
30 107 41.2 19 4 US-08-449-728-2 Sequence 2, Appli  
31 107 41.2 20 2 US-08-640-344-1 Sequence 1, Appli  
32 107 41.2 20 2 US-08-640-344-3 Sequence 3, Appli  
33 107 41.2 20 2 US-08-640-344-5 Sequence 5, Appli  
34 107 41.2 20 2 US-08-640-344-7 Sequence 7, Appli  
35 107 41.2 20 2 US-08-468-540B-7 Sequence 7, Appli  
36 107 41.2 20 4 US-08-960-190A-28 Sequence 28, Appli  
37 103.5 39.8 26 1 US-08-227-372-2 Sequence 2, Appli  
38 103.5 39.8 26 3 US-08-470-397-2 Sequence 3, Appli  
39 102 39.2 20 1 US-08-227-372-3 Sequence 2, Appli  
40 102 39.2 20 2 US-08-468-540B-8 Sequence 8, Appli  
41 102 39.2 20 3 US-08-470-397-3 Sequence 3, Appli  
42 101 38.8 18 2 US-08-468-540B-17 Sequence 17, Appli  
43 100 38.5 19 2 US-08-468-540B-18 Sequence 18, Appli  
44 100 38.5 19 2 US-08-468-540B-24 Sequence 24, Appli  
45 96 36.9 17 2 US-08-468-540B-19 Sequence 19, Appli

#### ALIGNMENTS

RESULT 1  
US-08-327-357A-1  
; Sequence 1, Application US/08327357A  
; Patent No. 5817629  
; GENERAL INFORMATION:  
; APPLICANT: WARREN, Kenneth G.  
; APPLICANT: CATZ, Ingrid  
; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC  
; TITLE OF INVENTION: PROTEIN AND THE ADMINISTRATION OF MYELIN BASIC PROTEIN  
; TITLE OF INVENTION: PEPTIDES TO MULTIPLE SCLEROSIS PATIENTS  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
; STREET: 1201 New York Avenue, N.W., Suite 1000  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/327,357A  
; FILING DATE: 21-OCT-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/798,099  
; FILING DATE: 27-NOV-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: CA 2,053,799-0  
; FILING DATE: 22-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Innen, Jeffrey L.  
; REGISTRATION NUMBER: 28,957  
; REFERENCE/DOCKET NUMBER: 27052-115469  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-962-4810  
; TELEFAX: 202-962-8300  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 170 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; IMMEDIATE SOURCE:

CLONE: human myelin basic protein  
US-08-327-357A-1

Query Match 100.0%; Score 260; DB 2; Length 170;  
Best Local Similarity 100.0%; Pred. No. 2.1e-27;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLSPQKSHGRTQDENPVVHFFKNIVTPTPTPPSQGK 46  
|||||  
DB 61 HHPARTAHYGLSPQKSHGRTQDENPVVHFFKNIVTPTPTPPSQGK 106

RESULT 2  
US-09-007-520-1  
; Sequence 1, Application US/09007520  
; Patent No. 6103696  
; GENERAL INFORMATION:  
; APPLICANT: WARREN, Kenneth G.  
; APPLICANT: CATZ, Ingrid  
; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC  
; TITLE OF INVENTION: PROTEIN AND THE ADMINISTRATION OF MYELIN BASIC PROTEIN  
; TITLE OF INVENTION: PEPTIDES TO MUTIPLE SCLEROSIS PATIENTS  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
; STREET: 1201 New York Avenue, N.W., Suite 1000  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/007,520  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/327,357  
; FILING DATE:  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: CA 2,053,799-0  
; FILING DATE: 22-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ihnen, Jeffrey L.  
; REGISTRATION NUMBER: 28,957  
; REFERENCE/DOCKET NUMBER: 27052-115469  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-962-4810  
; TELEFAX: 202-962-8300  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 170 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; IMMEDIATE SOURCE:  
; CLONE: human myelin basic protein  
US-09-007-520-1

Query Match 100.0%; Score 260; DB 3; Length 170;  
Best Local Similarity 100.0%; Pred. No. 2.1e-27;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLSPQKSHGRTQDENPVVHFFKNIVTPTPTPPSQGK 46  
|||||

DB 61 HHPARTAHYGLSPQKSHGRTQDENPVVHFFKNIVTPTPTPPSQGK 106

RESULT 3  
US-09-055-263-1  
; Sequence 1, Application US/09055263  
; Patent No. 625040  
; GENERAL INFORMATION:  
; APPLICANT: WARREN, Kenneth G.  
; APPLICANT: CATZ, Ingrid  
; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC  
; TITLE OF INVENTION: PROTEIN AND THE ADMINISTRATION OF MYELIN BASIC PROTEIN  
; TITLE OF INVENTION: PEPTIDES TO MUTIPLE SCLEROSIS PATIENTS  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
; STREET: 1201 New York Avenue, N.W., Suite 1000  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/055,263  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/327,357  
; FILING DATE: 21-OCT-1994  
; APPLICATION NUMBER: US 07/798,099  
; FILING DATE: 27-NOV-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: CA 2,053,799-0  
; FILING DATE: 22-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ihnen, Jeffrey L.  
; REGISTRATION NUMBER: 28,957  
; REFERENCE/DOCKET NUMBER: 27052-115469  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-962-4810  
; TELEFAX: 202-962-8300  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 170 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; IMMEDIATE SOURCE:  
; CLONE: human myelin basic protein  
US-09-055-263-1

Query Match 100.0%; Score 260; DB 4; Length 170;  
Best Local Similarity 100.0%; Pred. No. 2.1e-27;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLSPQKSHGRTQDENPVVHFFKNIVTPTPTPPSQGK 46  
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DB 61 HHPARTAHYGLSPQKSHGRTQDENPVVHFFKNIVTPTPTPPSQGK 106

RESULT 4  
US-09-007-520-1  
; Sequence 1, Application US/09007520  
; Patent No. 6258781  
; GENERAL INFORMATION:

APPLICANT: WARREN, Kenneth G.  
CATZ, Ingrid  
TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC  
PROTEIN AND THE ADMINISTRATION OF MYELIN BASIC PROTEIN  
PEPTIDES TO MULTIPLE SCLEROSIS PATIENTS  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue, N.W., Suite 1000  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/007,520  
FILING DATE: 15-Jan-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/327,357  
FILING DATE: <Unknown>  
APPLICATION NUMBER: CA 2,053,799-0  
FILING DATE: 22-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 27052-1115469  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 170 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: human myelin basic protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-007-520-1  
Query Match 100.0%; Score 260; DB 4; Length 170;  
Best Local Similarity 100.0%; Pred. No. 2.1e-27;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HHPARTAHYGLPQKSHGRQTQDENPVVHFFKNIVTPRTPPPSQGK 46  
Db 61 HHPARTAHYGLPQKSHGRQTQDENPVVHFFKNIVTPRTPPPSQGK 106  
RESULT 5  
US-09-342-408B-2  
Sequence 2, Application US/08342408B  
Patent No. 6329499  
GENERAL INFORMATION:  
APPLICANT: Ling, Nicholas  
APPLICANT: Gaur, Amitabh  
APPLICANT: Conlon, Paul J.  
APPLICANT: Steinman, Lawrence  
TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE  
SCLEROSIS USING PEPTIDE ANALOGUES OF HUMAN MYELIN BASIC  
PROTEIN  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/342,408B  
FILING DATE: 18-NOV-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6329499tenburg, Carol  
REGISTRATION NUMBER: 39,317  
REFERENCE/DOCKET NUMBER: 690068.405  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 170 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-342-408B-2  
Query Match 100.0%; Score 260; DB 4; Length 170;  
Best Local Similarity 100.0%; Pred. No. 2.1e-27;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HHPARTAHYGLPQKSHGRQTQDENPVVHFFKNIVTPRTPPPSQGK 46  
Db 61 HHPARTAHYGLPQKSHGRQTQDENPVVHFFKNIVTPRTPPPSQGK 106  
RESULT 6  
US-08-781-122-2  
Sequence 2, Application US/08781122  
Patent No. 5948764  
GENERAL INFORMATION:  
APPLICANT: Gaur, Amitabh  
APPLICANT: Conlon, Paul J.  
APPLICANT: Ling, Nicholas  
TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS  
UTILIZING PEPTIDE ANALOGUES OF HUMAN MYELIN BASIC PROTEIN  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/781,122  
FILING DATE: 09-JAN-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 690068.418C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 171 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-781-122-2

Query Match 100.0%; Score 260; DB 2; Length 171;  
Best Local Similarity 100.0%; Pred. No. 2.le-27;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLSPQKSHGRQTQDENPVVHFFKNIIVTRTPPPSQGK 46  
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Db 62 HHPARTAHYGLSPQKSHGRQTQDENPVVHFFKNIIVTRTPPPSQGK 107

## RESULT 7

US-09-137-759-2  
; Sequence 2, Application US/09137759  
; Patent No. 6251396

; GENERAL INFORMATION:  
; APPLICANT: Gaur, Amitabh

; APPLICANT: Conlon, Paul J.  
; APPLICANT: Ling, Nicholas C.

; APPLICANT: Staehlin, Theophil  
; APPLICANT: Crowe, Paul D.

; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING  
; TITLE OF INVENTION: PEPTIDE ANALOGS OF HUMAN MYELIN BASIC PROTEIN  
; FILE REFERENCE: 690068.409C1

; CURRENT APPLICATION NUMBER: US/09/137,759  
; CURRENT FILING DATE: 1998-08-20

; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2  
; LENGTH: 171

; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-137-759-2

Query Match 100.0%; Score 260; DB 4; Length 171;  
Best Local Similarity 100.0%; Pred. No. 2.le-27;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLSPQKSHGRQTQDENPVVHFFKNIIVTRTPPPSQGK 46  
|||  
Db 62 HHPARTAHYGLSPQKSHGRQTQDENPVVHFFKNIIVTRTPPPSQGK 107

## RESULT 8

5194425-4  
; Patent No. 5194425

; APPLICANT: SHARMA, SOMESH D.; LERCH, L. BERNARD; CLARK,  
; BRIAN R.

; TITLE OF INVENTION: MHC-MEDIATED TOXIC CONJUGATES USEFUL IN  
; AMELIORATING AUTOIMMUNITY

; NUMBER OF SEQUENCES: 9  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/367,751  
; FILING DATE: 21-JUN-1989

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 210,594

; FILING DATE: 23-JUN-1988  
; SEQ ID NO: 4;

; LENGTH: 168  
5194425-4

Query Match 90.0%; Score 234; DB 6; Length 168;  
Best Local Similarity 93.5%; Pred. No. 6.le-24;  
Matches 43; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLSPQKSHGRQTQDENPVVHFFKNIIVTRTPPPSQGK 46  
|||  
Db 59 HHAARTAHYGLSPQKSHGRQTQDENPVVHFFKNIIVTRTPPPSQGK 104

## RESULT 9

US-08-227-372-1

; Sequence 1, Application US/08227372  
; Patent No. 5763585

; GENERAL INFORMATION:  
; APPLICANT: Nag, Bishwajit

; TITLE OF INVENTION: PURIFICATION AND CHARACTERIZATION OF  
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEXES USEFUL IN AMELIORATING AUTOIMMUNITY

; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: Steuart Street Tower, One Market Plaza

; CITY: San Francisco  
; STATE: California

; COUNTRY: US  
; ZIP: 94105-1493

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/227,372  
; FILING DATE: 14-APR-1994

; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/136,216  
; FILING DATE: 13-OCT-1993

; ATTORNEY/AGENT INFORMATION:  
; NAME: Bastian, Kevin L.

; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 14058-32-1

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-9600

; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 170 amino acids

; TYPE: amino acid  
; MOLECULE TYPE: protein

; NAME/KEY: Protein  
; LOCATION: 1..170

; OTHER INFORMATION: /note= "Myelin basic protein"  
US-08-227-372-1

Query Match 84.8%; Score 220.5; DB 1; Length 170;  
Best Local Similarity 87.2%; Pred. No. 3.9e-22;  
Matches 41; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

Qy 1 HHPARTAHYGLSPQKSHG-RTQDENPVVHFFKNIIVTRTPPPSQGK 46  
|||  
Db 60 HHAARTAHYGLSPQKSHGRQTQDENPVVHFFKNIIVTRTPPPSQGK 106

## RESULT 10

US-08-462-351-3

; Sequence 3, Application US/08462351  
; Patent No. 6106840

; GENERAL INFORMATION:  
; APPLICANT: Sharma, Somesh D.

; APPLICANT: Clark, Brian R.  
; APPLICANT: Lerch, Bernard L.

; TITLE OF INVENTION: MHC Conjugates Useful in Ameliorating  
; TITLE OF INVENTION: Autoimmunity







Query Match 84.4%; Score 219.5; DB 3; Length 170;  
Best Local Similarity 87.2%; Pred. No. 5.3e-22;  
Matches 41; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 HHPARTAHYGLSPQKSHG-RTQDENPVVHFFKNIIVTPTPPPSQK 46  
DB 60 HHAARTXHYGLSPQKXGHRXDENPVVHFFKNIIVTPTPPPSQK 106

## RESULT 13

US-08-297-395-2  
; Sequence 2, Application US/08297395A  
; Patent No. 6039947  
; GENERAL INFORMATION:  
; APPLICANT: Howard L. Weiner  
; APPLICANT: David A. Hafner  
; TITLE OF INVENTION: PEPTIDES DERIVED FROM IMMUNODOMINANT  
; TITLE OF INVENTION: EPITOPES OF MYELIN BASIC PROTEIN  
; FILE REFERENCE: 1010/057230S3  
; CURRENT APPLICATION NUMBER: US/08/297,395A  
; CURRENT FILING DATE: 1994-08-11  
; EARLIER APPLICATION NUMBER: 08/059,189  
; EARLIER FILING DATE: 1993-05-06  
; EARLIER APPLICATION NUMBER: 07/502,559  
; EARLIER FILING DATE: 1990-03-30  
; EARLIER APPLICATION NUMBER: PCT/US88/02139  
; EARLIER FILING DATE: 1988-06-24  
; EARLIER APPLICATION NUMBER: 07/065,734  
; EARLIER FILING DATE: 1987-06-24  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 40  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-297-395-2

Query Match 76.2%; Score 198; DB 3; Length 40;  
Best Local Similarity 100.0%; Pred. No. 7.1e-20;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 SLQKSHGRQDENPVVHFFKNIIVTPTPPPSQK 46  
DB 1 SLQKSHGRQDENPVVHFFKNIIVTPTPPPSQK 36

## RESULT 14

5468481-3  
; Patent No. 5468481  
; APPLICANT: SHARMA, SOMESH D.; CLARK, BRIAN R.; LERCH, BERNARD L.  
; TITLE OF INVENTION: MHC CLASS II-PEPTIDE CONJUGATES USEFUL  
; IN AMELIORATING AUTOIMMUNITY  
; NUMBER OF SEQUENCES: 7  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/869,293  
; FILING DATE: 14-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 690,840  
; FILING DATE: 23-APR-1991  
; APPLICATION NUMBER: 576,084  
; FILING DATE: 30-AUG-1990  
; APPLICATION NUMBER: 210,594  
; FILING DATE: 23-JUN-1988  
; APPLICATION NUMBER: 635,840  
; FILING DATE: 28-DEC-1998  
; APPLICATION NUMBER: 367,751  
; FILING DATE: 21-JUN-1989  
; SEQ ID NO: 3  
; LENGTH: 170  
5468481-3

Query Match 75.2%; Score 195.5; DB 6; Length 170;  
Best Local Similarity 83.3%; Pred. No. 8.4e-19;  
Matches 40; Conservative 0; Mismatches 5; Indels 3; Gaps 3;  
QY 1 HHPARTAHYGLSPQKSHG-RTQDENPVVHFFKNIIVTPTPPPSQK 46  
DB 60 HHAARTXHYGLSPQKXGHRXDENPVVHFFKNIIVTPTPPPSQK 106

## RESULT 15

US-08-480-190-46  
; Sequence 46, Application US/08480190  
; Patent No. 5827516  
; GENERAL INFORMATION:  
; APPLICANT: Robert G. Urban  
; APPLICANT: Roman M. Chicz  
; APPLICANT: Dario A. A. Vignali  
; APPLICANT: Mary L. Hedley  
; APPLICANT: Lawrence J. Stern  
; APPLICANT: Jack L. Strominger  
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
; NUMBER OF SEQUENCES: 274  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480,190  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/077,255  
; FILING DATE: June 15, 1993  
; APPLICATION NUMBER: 07/925,460  
; FILING DATE: August 11, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00246/168001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 46:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 24  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-480-190-46

Query Match 51.9%; Score 135; DB 2; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1e-11;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GRQDENPVVHFFKNIIVTPTPP 24

Search completed: August 28, 2002, 16:35:30  
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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.  
OM protein - protein search, using sw model  
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(without alignments)  
78.877 Million cell updates/sec

Title: US-09-813-383-1  
Perfect score: 260  
Sequence: 1 HHPARTAHYGLPQKSHGRT.....VHFFKNIVTPRPPSQGK 46

Scoring table:  
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Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs., 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0  
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# SUMMARIES

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2	260	100.0	108	21	US-09-760-443-1465
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4	260	100.0	170	3	US-07-798-099A-1
5	260	100.0	170	6	US-08-241-246A-1
6	260	100.0	170	6	US-08-241-246B-1
7	260	100.0	170	7	US-08-327-357-1

8	260	100.0	170	7	US-08-328-224-5	Sequence 5, Appli
9	260	100.0	170	7	US-08-342-078-2	Sequence 2, Appli
10	260	100.0	170	8	US-08-404-228-1	Sequence 1, Appli
11	260	100.0	170	8	US-08-462-941A-1	Sequence 1, Appli
12	260	100.0	170	8	US-08-463-412-1	Sequence 1, Appli
13	260	100.0	170	8	US-08-463-456-1	Sequence 1, Appli
14	260	100.0	170	8	US-08-481-938-1	Sequence 1, Appli
15	260	100.0	170	24	US-10-015-540-2	Sequence 2, Appli
16	260	100.0	171	1	PCT-US00-06233-4	Sequence 4, Appli
17	260	100.0	171	7	US-08-342-078A-2	Sequence 2, Appli
18	260	100.0	171	8	US-08-484-403-2	Sequence 2, Appli
19	260	100.0	171	13	US-08-953-937-2	Sequence 12, Appli
20	260	100.0	171	16	US-09-218-277-12	Sequence 4, Appli
21	260	100.0	171	16	US-09-267-590-4	Sequence 12, Appli
22	260	100.0	171	17	US-09-314-161-12	Sequence 2, Appli
23	260	100.0	171	17	US-09-378-244-2	Sequence 12, Appli
24	260	100.0	171	22	US-09-893-348-12	Sequence 4, Appli
25	260	100.0	171	23	US-09-947-770-4	Sequence 2, Appli
26	260	100.0	171	23	US-09-989-476-2	Sequence 12, Appli
27	260	100.0	171	24	US-10-000-439-12	Sequence 13007, A
28	260	100.0	176	1	PCT-US01-14827-13007	Sequence 9330, Ap
29	260	100.0	183	1	PCT-US01-08656-9330	Sequence 28, Appli
30	260	100.0	186	17	US-09-310-707A-28	Sequence 54, Appli
31	260	100.0	197	19	US-09-512-563-54	Sequence 54, Appli
32	260	100.0	197	19	US-09-512-563A-54	Sequence 1, Appli
33	260	100.0	197	19	US-09-512-563C-54	Sequence 1502, Ap
34	260	100.0	203	18	US-09-463-186-1	Sequence 1779, Ap
35	260	100.0	315	21	US-09-760-443-1502	Sequence 13008, A
36	260	100.0	315	21	US-09-760-446A-1779	Sequence 3, Appli
37	260	100.0	325	1	PCT-US01-14827-13008	Sequence 4, Appli
38	254	97.7	167	3	US-07-987-751-3	Sequence 1, Appli
39	254	97.7	168	3	US-07-987-751-4	Sequence 2, Appli
40	252	96.9	170	5	US-07-798-099-1	Sequence 7, Appli
41	233.5	89.8	170	5	US-08-136-216-2	Sequence 5, Appli
42	232	89.2	168	3	US-07-987-751-7	Sequence 6, Appli
43	226.5	87.1	169	3	US-07-987-751-5	Sequence 1, Appli
44	226.5	87.1	172	3	US-07-987-751-6	Sequence 1, Appli
45	220.5	84.8	170	5	US-08-136-216-1	

## ALIGNMENTS

RESULT 1  
US-09-813-383-1  
; Sequence 1, Application US/09813383  
; GENERAL INFORMATION:  
; APPLICANT: WARREN, KENNETH G.  
; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC PROTEIN AND  
; TITLE OF INVENTION: THE ADMINISTRATION OF MYELIN BASIC PROTEIN PEPTIDES TO  
; TITLE OF INVENTION: MULTIPLE SCLEROSIS PATIENTS  
; FILE REFERENCE: 098810/027 87A1  
; CURRENT APPLICATION NUMBER: US/09/813,383  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 46  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-09-813-383-1

Query Match 100.0% Score 260; DB 22; Length 46;  
Best Local Similarity 100.0%; Pred. No. 3.2e-25;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIVTPRPPSQGK 46  
|||||  
Db 1 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIVTPRPPSQGK 46  
|||||



FILING DATE: 15-MAY-1992  
 APPLICATION NUMBER: 07/857,331  
 FILING DATE: 25-MARCH-1992  
 APPLICATION NUMBER: 07/662,276  
 FILING DATE: 28-FEBRUARY-1991  
 APPLICATION NUMBER: 07/431,565  
 FILING DATE: 11-MARCH-1989  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragouras, Amy E.  
 REGISTRATION NUMBER: 36,207  
 REFERENCE/DOCKET NUMBER: IMI-053 (084.00S)  
 TELEPHONE: (617) 227-7400  
 TELEFAX: (617) 227-5941  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 170 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-241-246-1

Query Match 100.0%; Score 260; DB 6; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-24;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIIVTPTPPPSQKKG 46  
 Db 61 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIIVTPTPPPSQKKG 106

RESULT 6  
 US-08-241-246B-1  
 Sequence 1, Application US/08241246B  
 GENERAL INFORMATION:  
 APPLICANT: Smilek, Dawn; Hsu, Di-Hwei; and Shi, Jia-Dong  
 TITLE OF INVENTION: COMPOSITIONS AND TREATMENT FOR  
 TITLE OF INVENTION: MULTIPLE SCLEROSIS  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD, LLP  
 STREET: 28 State Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: ASCII-text  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/241,246B  
 FILING DATE: 10-MAY-1994  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/006,116  
 FILING DATE: 15-JANUARY-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragouras, Amy E.  
 REGISTRATION NUMBER: 36,207  
 REFERENCE/DOCKET NUMBER: IMI-053 (084.00S)  
 TELEPHONE: (617) 227-7400  
 TELEFAX: (617) 742-4214  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 170 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: Internal

US-08-241-246B-1

Query Match 100.0%; Score 260; DB 6; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-24;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIIVTPTPPPSQKKG 46  
 Db 61 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIIVTPTPPPSQKKG 106

RESULT 7  
 US-08-327-357-1  
 Sequence 1, Application US/08327357  
 GENERAL INFORMATION:  
 APPLICANT: WARREN, Kenneth G.  
 APPLICANT: CATZ, Ingrid  
 TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN  
 TITLE OF INVENTION: BASIC PROTEIN AND THE ADMINISTRATION OF MYELIN BASIC  
 TITLE OF INVENTION: PROTEIN PEPTIDES TO MULTIPLE SCLEROSIS PATIENTS  
 NUMBER OF SEQUENCES: 1  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
 STREET: 1201 New York Avenue, N.W.  
 CITY: Washington, D.C.  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005-3917  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/327,357  
 FILING DATE: 21-OCT-1994  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: CA 2,053,799-0  
 FILING DATE: 22-OCT-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Jeffrey L. Innes  
 REGISTRATION NUMBER: 28,957  
 REFERENCE/DOCKET NUMBER: 18760-95536(temp)  
 TELEPHONE: (202)962-4800  
 TELEFAX: (202)962-8300  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 170 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ORIGINAL SOURCE:  
 ORGANISM: homo sapien  
 IMMEDIATE SOURCE:  
 CLONE: human myelin basic protein  
 US-08-327-357-1

Query Match 100.0%; Score 260; DB 7; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-24;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIIVTPTPPPSQKKG 46  
 Db 61 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIIVTPTPPPSQKKG 106

RESULT 8  
 US-08-328-224-5

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; Sequence 5, Application US/08328224
; GENERAL INFORMATION:
; APPLICANT: Smilek, Dawn
; APPLICANT: Samson, Michael
; APPLICANT: Gifter, Malcolm
; APPLICANT: Hsu, Di-Hwei
; APPLICANT: Shi, Jia-Dong
; APPLICANT: Pallard, Xavier
; APPLICANT: Devaux, Brigitte
; APPLICANT: Rothbard, Jonathan
; APPLICANT: Franzen, Henry M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ADMINISTERING TO HUMANS SUFFERIN
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,224
; FILING DATE: 10-25-94
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: 094.0 US (IMI-056)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
; US-08-328-224-5

Query Match 100.0%; Score 260; DB 7; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.6e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLPKSHGRGTQDENPVVHFFKNIVTPTPTPPSQKG 46
Db 61 HHPARTAHYGLPKSHGRGTQDENPVVHFFKNIVTPTPTPPSQKG 106

RESULT 9
US-08-342-078-2
; Sequence 2, Application US/08342078
; GENERAL INFORMATION:
; APPLICANT: Steinman, Lawrence
; APPLICANT: Ling, Nicholas
; APPLICANT: Conlon, Paul J.
; APPLICANT: Gaur, Amitabh
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE
; TITLE OF INVENTION: SCLEROSIS USING PEPTIDE ANALOGUES AT POSITION 91 OF HUMAN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA

; Sequence 1, Application US/08404228
; GENERAL INFORMATION:
; APPLICANT: Smilek, Dawn
; APPLICANT: Samson, Michael F.;
; APPLICANT: Gifter, Malcolm;
; APPLICANT: Hsu, Di-Hwei;
; APPLICANT: Shi, Jia-Dong;
; APPLICANT: Pallard, Xavier;
; APPLICANT: Devaux, Brigitte;
; APPLICANT: Rothbard, Jonathan; and
; APPLICANT: Franzen, Henry M.
; TITLE OF INVENTION: Compositions and Treatment for Multiple
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/404,228
; FILING DATE: 15-March-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Anne I. Craig
; REGISTRATION NUMBER: Reg. No. 32, 976
; REFERENCE/DOCKET NUMBER: 094.1 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
```

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; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/342,078
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Nottenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 690068.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANDBERRY
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-342-078-2

Query Match 100.0%; Score 260; DB 7; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.6e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLPKSHGRGTQDENPVVHFFKNIVTPTPTPPSQKG 46
Db 61 HHPARTAHYGLPKSHGRGTQDENPVVHFFKNIVTPTPTPPSQKG 106

RESULT 10
US-08-404-228-1
; Sequence 1, Application US/08404228
; GENERAL INFORMATION:
; APPLICANT: Smilek, Dawn
; APPLICANT: Samson, Michael F.;
; APPLICANT: Gifter, Malcolm;
; APPLICANT: Hsu, Di-Hwei;
; APPLICANT: Shi, Jia-Dong;
; APPLICANT: Pallard, Xavier;
; APPLICANT: Devaux, Brigitte;
; APPLICANT: Rothbard, Jonathan; and
; APPLICANT: Franzen, Henry M.
; TITLE OF INVENTION: Compositions and Treatment for Multiple
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/404,228
; FILING DATE: 15-March-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Anne I. Craig
; REGISTRATION NUMBER: Reg. No. 32, 976
; REFERENCE/DOCKET NUMBER: 094.1 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
```

TELEFAX: (617) 466-6010  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 170 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FRAGMENT TYPE: internal  
 US-08-404-228-1

Query Match 100.0% Score 260; DB 8; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-24;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYSLPQKSHGRQTODENPVVHFFKNIVTPTPPPSQKGG 46  
 Db 61 HHPARTAHYSLPQKSHGRQTODENPVVHFFKNIVTPTPPPSQKGG 106

RESULT 11

US-08-462-941A-1  
 ; Sequence 1, Application US/08462941A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Smilek, Dawn;  
 ; APPLICANT: Samson, Michael F.;  
 ; APPLICANT: Geffer, Malcolm;  
 ; APPLICANT: Hsu, Di-Hwei;  
 ; APPLICANT: Shi, Jia-Dong;  
 ; APPLICANT: Pallard, Xavier;  
 ; APPLICANT: Devaux, Brigitte;  
 ; APPLICANT: Rothbard, Jonathan; and  
 ; APPLICANT: Franzen, Henry M.  
 ; TITLE OF INVENTION: Sclerosis  
 ; NUMBER OF SEQUENCES: 71  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: LAHIVE & COCKFIELD  
 ; STREET: 60 State Street, Suite 510  
 ; CITY: Boston  
 ; STATE: Massachusetts  
 ; COUNTRY: USA  
 ; ZIP: 02109-1875  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/462.941A  
 ; FILING DATE: 5-June-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/404,228  
 ; FILING DATE: 15-March-1995  
 ; APPLICATION NUMBER: US 08/328,224  
 ; FILING DATE: 25-October-1994  
 ; APPLICATION NUMBER: US 08/300,811  
 ; FILING DATE: 1-September-1994  
 ; APPLICATION NUMBER: US 08/241,246  
 ; FILING DATE: 10-May-1994  
 ; APPLICATION NUMBER: US 08/116,824  
 ; FILING DATE: 3-September-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Amy E. Mandragouras  
 ; REGISTRATION NUMBER: Reg. No. 36,207  
 ; REFERENCE/DOCKET NUMBER: 094.1 US01 (IMI-052CPDV)  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (617) 227-7400  
 ; TELEFAX: (617) 227-5941  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 170 amino acids  
 ; TYPE: amino acid

TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FRAGMENT TYPE: internal  
 US-08-462-941A-1

Query Match 100.0% Score 260; DB 8; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-24;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYSLPQKSHGRQTODENPVVHFFKNIVTPTPPPSQKGG 46  
 Db 61 HHPARTAHYSLPQKSHGRQTODENPVVHFFKNIVTPTPPPSQKGG 106

RESULT 12

US-08-463-412-1  
 ; Sequence 1, Application US/08463412  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Smilek, Dawn;  
 ; APPLICANT: Samson, Michael F.;  
 ; APPLICANT: Geffer, Malcolm;  
 ; APPLICANT: Hsu, Di-Hwei;  
 ; APPLICANT: Shi, Jia-Dong;  
 ; APPLICANT: Pallard, Xavier;  
 ; APPLICANT: Devaux, Brigitte;  
 ; APPLICANT: Rothbard, Jonathan; and  
 ; APPLICANT: Franzen, Henry M.  
 ; TITLE OF INVENTION: Compositions and Treatment for Multiple Sclerosis  
 ; NUMBER OF SEQUENCES: 71  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: LAHIVE & COCKFIELD  
 ; STREET: 60 State Street, Suite 510  
 ; CITY: Boston  
 ; STATE: Massachusetts  
 ; COUNTRY: USA  
 ; ZIP: 02109-1875  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/463.412  
 ; FILING DATE: 5-June-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/404,228  
 ; FILING DATE: 15-March-1995  
 ; APPLICATION NUMBER: US 08/328,224  
 ; FILING DATE: 25-October-1994  
 ; APPLICATION NUMBER: US 08/300,811  
 ; FILING DATE: 1-September-1994  
 ; APPLICATION NUMBER: US 08/241,246  
 ; FILING DATE: 10-May-1994  
 ; APPLICATION NUMBER: US 08/116,824  
 ; FILING DATE: 3-September-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Amy E. Mandragouras  
 ; REGISTRATION NUMBER: Reg. No. 36,207  
 ; REFERENCE/DOCKET NUMBER: 094.1 USD2 (IMI-052DV2)  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (617) 227-7400  
 ; TELEFAX: (617) 227-5941  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 170 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; FRAGMENT TYPE: internal  
 ; US-08-463-412-1





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: GENERAL INFORMATION:
: APPLICANT: Ling, Nicholas
: Gaur, Amitabh
: Conlon, Paul J.
: Steinman, Lawrence
: TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE
: SCLEROSIS USING PEPTIDE ANALOGUES OF HUMAN MYELIN BASIC
: PROTEIN
:
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Seed Intellectual Property Law Group PLLC
: STREET: 701 Fifth Avenue, Suite 6300
: CITY: Seattle
: STATE: Washington
: COUNTRY: USA
: ZIP: 98104-7092
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/015,540
: FILING DATE: 11-Dec-2001
: CLASSIFICATION: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Christiansen, William T.
: REGISTRATION NUMBER: 44,614
: REFERENCE/DOCKET NUMBER: 690068.405C3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 622-4900
: TELEFAX: (206) 682-6031
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 170 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-015-540-2

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Query Match      100.0%; Score 260; DB 24; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.6e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGSILPOKSHGRQTQDENPVWHFFKNIVTPRTPPPSOGKG 46
   ||||||||||||||||||||||||||||||||||||||||||||
Db 61 HHPARTAHYGSILPOKSHGRQTQDENPVWHFFKNIVTPRTPPPSOGKG 106

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Search completed: August 28, 2002, 16:39:34  
Job time: 346 sec





US-10-143-775-898

Query Match 100.0%; Score 260; DB 6; Length 108;  
Best Local Similarity 100.0%; Pred. No. 3.2e-24;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIIVTPTPPPSQKG 46  
|||||  
Db 11 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIIVTPTPPPSQKG 56

RESULT 3

US-10-212-054-1465  
; Sequence 1465, Application US/10212054  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: P21212CIN  
; CURRENT APPLICATION NUMBER: US/10/212,054  
; CURRENT FILING DATE: 2002-08-06  
; NUMBER OF SEQ ID NOS: 2164  
; Prior application removed - See File Wrapper or Palm  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1465  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-212-054-1465

Query Match 100.0%; Score 260; DB 6; Length 108;  
Best Local Similarity 100.0%; Pred. No. 3.2e-24;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIIVTPTPPPSQKG 46  
|||||  
Db 11 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIIVTPTPPPSQKG 56

RESULT 4

PCT-US02-13527-12  
; Sequence 12, Application PC/TUS0213527  
; GENERAL INFORMATION:  
; APPLICANT: Regents of the University of California  
; APPLICANT: Saxon, Andrew  
; APPLICANT: Zhang, Ke  
; APPLICANT: Zhu, Daoheng  
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR  
; FILE REFERENCE: UC067.004QPC  
; CURRENT APPLICATION NUMBER: PCT/US02/13527  
; CURRENT FILING DATE: 2002-05-01  
; PRIOR APPLICATION NUMBER: US 09/847,208  
; PRIOR FILING DATE: 2001-05-01  
; PRIOR APPLICATION NUMBER: US 10/000,439  
; PRIOR FILING DATE: 2001-10-24  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 171  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US02-13527-12

Query Match 100.0%; Score 260; DB 1; Length 171;  
Best Local Similarity 100.0%; Pred. No. 5.6e-24;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIIVTPTPPPSQKG 46  
|||||  
Db 62 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIIVTPTPPPSQKG 107

RESULT 5

US-10-104-973-2  
; Sequence 2, Application US/10104973  
; GENERAL INFORMATION:  
; APPLICANT: Gaur, Amitabh  
; APPLICANT: Conlon, Paul J.  
; APPLICANT: Ling, Nicholas C.  
; APPLICANT: Staehlin, Theophil  
; APPLICANT: Crowe, Paul D.  
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING  
; FILE REFERENCE: 690068.405C4  
; CURRENT APPLICATION NUMBER: US/10/104,973  
; CURRENT FILING DATE: 2002-03-20  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 171  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-104-973-2

Query Match 100.0%; Score 260; DB 6; Length 171;  
Best Local Similarity 100.0%; Pred. No. 5.6e-24;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIIVTPTPPPSQKG 46  
|||||  
Db 62 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIIVTPTPPPSQKG 107

RESULT 6

US-08-431-644B-4  
; Sequence 4, Application US/08431644B  
; GENERAL INFORMATION:  
; APPLICANT: Nye, Steven H.  
; APPLICANT: Lenardo, Michael J.  
; APPLICANT: McFarland, Henry F.  
; APPLICANT: Matis, Louis A.  
; APPLICANT: Mueller, Eileen E.  
; APPLICANT: Mueller, John P.  
; APPLICANT: Pelfrey, Clara M.  
; APPLICANT: Squinto, Stephen P.  
; APPLICANT: Wilkins, James A.  
; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES  
; FILE REFERENCE: 1087-48(27)  
; CURRENT APPLICATION NUMBER: US/08/431,644B  
; CURRENT FILING DATE: 1995-05-02  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 172  
; TYPE: PRT  
; ORGANISM: human  
US-08-431-644B-4

Query Match 100.0%; Score 260; DB 4; Length 172;  
Best Local Similarity 100.0%; Pred. No. 5.6e-24;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIIVTPTPPPSQKG 46  
|||||  
Db 63 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIIVTPTPPPSQKG 108

RESULT 7

US-08-431-644C-4  
; Sequence 4, Application US/08431644C  
; GENERAL INFORMATION:

```

; APPLICANT: Nye, Steven H.
; APPLICANT: Lenardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matis, Louis A.
; APPLICANT: Mueller, Eileen E.
; APPLICANT: Mueller, John P.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES
; FILE REFERENCE: 1087-48(27)
; CURRENT APPLICATION NUMBER: US/08/431,644C
; CURRENT FILING DATE: 1995-05-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 172
; TYPE: PRT
; ORGANISM: human
US-08-431-644C-4

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```

Query Match      100.0%; Score 260; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 5.6e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 46
    |||||
Db 63 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 108
    |||||

```

```

RESULT 8
US-08-431-644B-1
; Sequence 1, Application US/08431644B
; GENERAL INFORMATION:
; APPLICANT: Nye, Steven H.
; APPLICANT: Lenardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matis, Louis A.
; APPLICANT: Mueller, Eileen E.
; APPLICANT: Mueller, John P.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES
; FILE REFERENCE: 1087-48(27)
; CURRENT APPLICATION NUMBER: US/08/431,644B
; CURRENT FILING DATE: 1995-05-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 197
; TYPE: PRT
; ORGANISM: human
US-08-431-644B-1

```

```

Query Match      100.0%; Score 260; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 6.6e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 46
    |||||
Db 88 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 133
    |||||

```

```

RESULT 9
US-08-431-644C-1
; Sequence 1, Application US/08431644C
; GENERAL INFORMATION:
; APPLICANT: Nye, Steven H.
; APPLICANT: Lenardo, Michael J.
; APPLICANT: McFarland, Henry F.

```

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; APPLICANT: Matis, Louis A.
; APPLICANT: Mueller, Eileen E.
; APPLICANT: Mueller, John P.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES
; FILE REFERENCE: 1087-48(27)
; CURRENT APPLICATION NUMBER: US/08/431,644C
; CURRENT FILING DATE: 1995-05-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 197
; TYPE: PRT
; ORGANISM: human
US-08-431-644C-1

```

```

Query Match      100.0%; Score 260; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 6.6e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 46
    |||||
Db 88 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 133
    |||||

```

```

RESULT 10
US-08-431-644B-2
; Sequence 2, Application US/08431644B
; GENERAL INFORMATION:
; APPLICANT: Nye, Steven H.
; APPLICANT: Lenardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matis, Louis A.
; APPLICANT: Mueller, Eileen E.
; APPLICANT: Mueller, John P.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES
; FILE REFERENCE: 1087-48(27)
; CURRENT APPLICATION NUMBER: US/08/431,644B
; CURRENT FILING DATE: 1995-05-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 203
; TYPE: PRT
; ORGANISM: human
US-08-431-644B-2

```

```

Query Match      100.0%; Score 260; DB 4; Length 203;
Best Local Similarity 100.0%; Pred. No. 6.8e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 46
    |||||
Db 88 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 133
    |||||

```

```

RESULT 11
US-08-431-644B-3
; Sequence 3, Application US/08431644B
; GENERAL INFORMATION:
; APPLICANT: Nye, Steven H.
; APPLICANT: Lenardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matis, Louis A.
; APPLICANT: Mueller, Eileen E.
; APPLICANT: Mueller, John P.

```

; APPLICANT: Pelfrey, Clara M.  
; APPLICANT: Squinto, Stephen P.  
; APPLICANT: Wilkins, James A.  
; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES  
; FILE REFERENCE: 1087-48(27)  
; CURRENT APPLICATION NUMBER: US/08/431,644B  
; CURRENT FILING DATE: 1995-05-02  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 203  
; TYPE: PRT  
; ORGANISM: human  
US-08-431-644B-3

Query Match 100.0%; Score 260; DB 4; Length 203;  
Best Local Similarity 100.0%; Pred. No. 6.8e-24;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 46  
|||||  
Db 88 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 133

RESULT 12  
US-08-431-644B-27  
; Sequence 27, Application US/08431644B  
; GENERAL INFORMATION:  
; APPLICANT: Nye, Steven H.  
; APPLICANT: Lenardo, Michael J.  
; APPLICANT: McFarland, Henry F.  
; APPLICANT: Matis, Louis A.  
; APPLICANT: Mueller, Eileen E.  
; APPLICANT: Mueller, John P.  
; APPLICANT: Pelfrey, Clara M.  
; APPLICANT: Squinto, Stephen P.  
; APPLICANT: Wilkins, James A.  
; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES  
; FILE REFERENCE: 1087-48(27)  
; CURRENT APPLICATION NUMBER: US/08/431,644B  
; CURRENT FILING DATE: 1995-05-02  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 27  
; LENGTH: 203  
; TYPE: PRT  
; ORGANISM: human  
US-08-431-644B-27

Query Match 100.0%; Score 260; DB 4; Length 203;  
Best Local Similarity 100.0%; Pred. No. 6.8e-24;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 46  
|||||  
Db 88 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 133

RESULT 13  
US-08-431-644C-2  
; Sequence 2, Application US/08431644C  
; GENERAL INFORMATION:  
; APPLICANT: Nye, Steven H.  
; APPLICANT: Lenardo, Michael J.  
; APPLICANT: McFarland, Henry F.  
; APPLICANT: Matis, Louis A.  
; APPLICANT: Mueller, Eileen E.  
; APPLICANT: Mueller, John P.  
; APPLICANT: Pelfrey, Clara M.  
; APPLICANT: Squinto, Stephen P.  
; APPLICANT: Wilkins, James A.

; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES  
; FILE REFERENCE: 1087-48(27)  
; CURRENT APPLICATION NUMBER: US/08/431,644C  
; CURRENT FILING DATE: 1995-05-02  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 203  
; TYPE: PRT  
; ORGANISM: human  
US-08-431-644C-2

Query Match 100.0%; Score 260; DB 4; Length 203;  
Best Local Similarity 100.0%; Pred. No. 6.8e-24;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 46  
|||||  
Db 88 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 133

RESULT 14  
US-08-431-644C-3  
; Sequence 3, Application US/08431644C  
; GENERAL INFORMATION:  
; APPLICANT: Nye, Steven H.  
; APPLICANT: Lenardo, Michael J.  
; APPLICANT: McFarland, Henry F.  
; APPLICANT: Matis, Louis A.  
; APPLICANT: Mueller, Eileen E.  
; APPLICANT: Mueller, John P.  
; APPLICANT: Pelfrey, Clara M.  
; APPLICANT: Squinto, Stephen P.  
; APPLICANT: Wilkins, James A.  
; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES  
; FILE REFERENCE: 1087-48(27)  
; CURRENT APPLICATION NUMBER: US/08/431,644C  
; CURRENT FILING DATE: 1995-05-02  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 203  
; TYPE: PRT  
; ORGANISM: human  
US-08-431-644C-3

Query Match 100.0%; Score 260; DB 4; Length 203;  
Best Local Similarity 100.0%; Pred. No. 6.8e-24;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 46  
|||||  
Db 88 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 133

RESULT 15  
US-08-431-644C-27  
; Sequence 27, Application US/08431644C  
; GENERAL INFORMATION:  
; APPLICANT: Nye, Steven H.  
; APPLICANT: Lenardo, Michael J.  
; APPLICANT: McFarland, Henry F.  
; APPLICANT: Matis, Louis A.  
; APPLICANT: Mueller, Eileen E.  
; APPLICANT: Mueller, John P.  
; APPLICANT: Pelfrey, Clara M.  
; APPLICANT: Squinto, Stephen P.  
; APPLICANT: Wilkins, James A.  
; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES  
; FILE REFERENCE: 1087-48(27)  
; CURRENT APPLICATION NUMBER: US/08/431,644C

; CURRENT FILING DATE: 1995-05-02  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 27  
; LENGTH: 203  
; TYPE: PRT  
; ORGANISM: human  
US-08-431-644C-27

Query Match 100.0%; Score 260; DB 4; Length 203;  
Best Local Similarity 100.0%; Pred. No. 6.8e-24;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 HHPARTAHYGSILPOKSHGRQTQDENPVVHFFKNIYVTRTPPPSOGKG 46  
Db 88 HHPARTAHYGSILPOKSHGRQTQDENPVVHFFKNIYVTRTPPPSOGKG 133

Search completed: August 28, 2002, 16:40:33  
Job time: 385 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2002, 16:33:08 ; Search time 25.27 seconds  
(without alignments)  
174.915 Million cell updates/sec

Title: US-09-813-383-1

Perfect score: 260  
Sequence: 1 HHPARTAHYGLPKSHGRT.....VHFKNIVTPPTPPSQGK 46

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_71.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	260	100.0	197	1 MBHUB	myelin basic prote
2	242	93.1	171	1 MBPGB	myelin basic prote
3	228.5	87.9	171	1 MBPGB	myelin basic prote
4	220.5	84.8	169	1 MBPGB	myelin basic prote
5	219.5	84.4	167	2 A37246	myelin basic prote
6	218.5	84.0	328	1 MBMSB	golli-myelin basic
7	204.5	78.7	128	1 MBRTS	myelin basic prote
8	181.5	69.8	174	2 S08535	myelin basic prote
9	116	44.6	42	2 B92087	myelin basic prote
10	80.5	31.0	155	2 B32999	myelin basic prote
11	78.5	30.2	128	2 A60215	myelin basic prote
12	77	29.6	14	2 S12904	protein kinase (PC
13	65.5	25.2	154	2 S55017	hypothetical prote
14	63	24.2	632	2 F83387	copper resistance
15	62	23.8	295	2 S58850	homeotic protein a
16	60	23.1	667	1 VCLJGL	env polyprotein pr
17	59	22.7	556	2 A81931	probable adhesin N
18	59	22.7	736	2 E71414	hypothetical prote
19	58.5	22.5	445	2 A56024	GDP dissociation i
20	56.5	21.7	159	2 AC2254	hypothetical prote
21	56.5	21.7	444	2 A55071	hydrogen peroxide-
22	56	21.5	562	2 T29858	hypothetical prote
23	55.5	21.3	218	2 F86939	probable lipoprote
24	55.5	21.3	263	2 A23659	spectrin beta chai
25	55.5	21.3	680	1 XJBVTK	transketolase (EC
26	55	21.2	257	2 D82350	ribonuclease PH VC
27	55	21.2	422	2 T09742	drought-induced pr
28	55	21.2	891	2 G82543	conserved hypothet
29	55	21.2	2061	2 T13751	transcription fact

## ALIGNMENTS

RESULT 1

MBHUB

myelin basic protein [validated] - human

N:Contains: myelin basic protein precursor, 17.2K splice form; myelin basic protein p

.5K splice form

C:Species: Homo sapiens (man)

C:Date: 18-Dec-1981 #sequence\_revision 25-Aug-1995 #text\_change 20-Apr-2001

C:Accession: S10482; A94106; B94106; A90256; JH0802; A60862; A61420; A33273; I54219;

R:Streichner, R.; Stoffel, W.

Biol. Chem. Hoppe-Seyler 370, 503-510, 1989

A:Title: The organization of the human myelin basic protein gene. Comparison with the

A:Reference number: S10482; MUID:89302693

A:Accession: S10482

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-197 <STR>

A:Cross-references: EMBL:X17286; NID:g34490; PIDN:CAA35179.1; PID:g1184244

R:Kamholz, J.; De Ferro, F.; Puckett, C.; Lazzarini, R.

Proc. Natl. Acad. Sci. U.S.A. 83, 4962-4966, 1986

A:Title: Identification of three forms of human myelin basic protein by cDNA cloning.

A:Reference number: A94106; MUID:86259714

A:Accession: A94106

A:Molecule type: mRNA

A:Residues: 1-59,86-197 <KAM>

A:Cross-references: GB:M13577; NID:g187408; PIDN:AAA59562.1; PID:g307160

A:Note: 18.5K splice form

A:Accession: B94106

A:Molecule type: mRNA

A:Residues: 1-197 <K2>

A:Note: antibody to the exon 2 encoded sequence detected a 21.5K splice form

A:Note: a 17.2K splice form is also described

A:Note: antibody to the exon 2 encoded sequence detected a 21.5K splice form; a 17.2K

Biochem. J. 123, 57-67, 1971

A:Title: Amino acid sequence of the encephalitogenic basic protein from human myelin.

A:Reference number: A90256; MUID:72066400

A:Accession: A90256

A:Molecule type: protein

A:Residues: 2-59,86-197 <CAR>

R:Proost, P.; Van Damme, J.; Opdenakker, G.

Biochem. Biophys. Res. Commun. 192, 1175-1181, 1993

A:Title: Leukocyte gelatinase B cleavage releases encephalitogens from human myelin b

A:Reference number: JH0802; MUID:93282820

A:Accession: JH0802

A:Molecule type: protein

A:Residues: 2-59,86-197 <PRO>

A:Experimental source: brain

R:Scoble, H.A.; Whitaker, J.N.; Biemann, K.

J. Neurochem. 47, 614-616, 1986

A:Title: Analysis of the primary sequence of human myelin basic protein peptides 1-44

A:Reference number: A60862; MUID:86280476

A:Accession: A60862

A:Molecule type: protein  
A:Residues: 2-45;117-197 <SCO>  
A:Note: evidence for acetylated amino end  
R:Gibson, B.W.; Gilliom, R.D.; Whitaker, J.N.; Biemann, K.  
J. Biol. Chem. 259, 5028-5031, 1984  
A:Title: Amino acid sequence of human myelin basic protein peptide 45-89 as determined by mass spectrometry  
A:Reference number: A61420; MUID:84185608  
A:Accession: A61420  
A:Molecule type: protein  
A:Residues: 46-59,86-116 <GIB>  
R:Wood, D.D.; Moscarello, M.A.  
J. Biol. Chem. 264, 5121-5127, 1989  
A:Title: The isolation, characterization, and lipid-aggregating properties of a citrulline-rich myelin basic protein  
A:Reference number: A33273; MUID:89174797  
A:Accession: A33273  
A:Molecule type: protein  
A:Residues: 15-25, 'X', 27-31, 'X', 33-59,86-148, 'X',150-156, 'X',158-185, 'X',187-196, 'X' <WAL>  
A:Note: form C-8; residues designated 'X' were determined as citrulline  
R:Baldwin, J. S.; Carnegie, P.R.  
Biochem. J. 123, 69-74, 1971  
A:Title: Isolation and partial characterization of methylated arginines from the encephalomyelinase  
A:Reference number: A90257; MUID:72066401  
A:Contents: annotation; methylarginine  
A:Note: Arg-134 may be unmodified, monomethylarginine, or dimethylarginine in the approx 139-149 region  
R:Lennon, V.A.; Wilks, A.V.; Carnegie, P.R.  
J. Immunol. 105, 1223-1230, 1970  
A:Reference number: A92806; MUID:71088405  
A:Contents: annotation  
A:Note: a region including residues 139-149 induces experimental autoimmune encephalomyelitis in mice  
R:Boylan, K.B.; Ayres, T.M.; Popko, B.; Takahashi, N.; Hood, L.E.; Prusiner, S.B.  
Genomics 6, 16-22, 1990  
A:Title: Repetitive DNA (TGG)n 5' to the human myelin basic protein gene: a new form of polyoma virus  
A:Reference number: I54219; MUID:90152679  
A:Accession: I54219  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-59 <RES>  
A:Cross-references: GB:M63599; NID:g187402; PIDN:AAA59560.1; PID:g187403  
R:Roth, H.J.; Kronquist, K.E.; Keriou de Rosbo, N.; Crandall, B.F.; Campagnoni, A.T.  
J. Neurosci. Res. 17, 321-328, 1987  
A:Title: Evidence for the expression of four myelin basic protein variants in the developing mouse brain  
A:Reference number: I56567; MUID:87311781  
A:Accession: I56567  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-132,144-197 <RE2>  
A:Cross-references: GB:M30516; NID:g187410; PIDN:AAA59563.1; PID:g307161  
A:Accession: I73634  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-197 <RE3>  
A:Cross-references: GB:M30515; NID:g187412; PIDN:AAA59564.1; PID:g307162  
R:Roth, H.J.; Kronquist, K.; Pretorius, P.J.; Crandall, B.F.; Campagnoni, A.T.  
J. Neurosci. Res. 16, 227-238, 1986  
A:Title: Isolation and characterization of a cDNA coding for a novel human 17.3K myelin protein  
A:Reference number: I56565; MUID:86308101  
A:Accession: I56565  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-59,86-133,145-197 <RE4>  
A:Cross-references: GB:M30047; NID:g187400; PIDN:AAA59559.1; PID:g307159  
R:Boullas, C.; Pang, H.; Mastroratti, F.; Moscarello, M.A.  
Arch. Biochem. Biophys. 322, 174-182, 1995  
A:Title: The isolation and characterization of four myelin basic proteins from the unbound myelin fraction  
A:Reference number: S66383; MUID:96004793  
A:Accession: S66383  
A:Molecule type: protein  
A:Residues: 23-25, 'X', 27-39 <BOU>  
C:Comment: Four alternatively spliced forms of myelin basic protein have been observed, C1, C2, C3, and C4  
C:Genetics:  
A:Gene: GDB:MBP  
A:Cross-references: GDB:119379; OMIM:159430  
A:Map position: 18q22-18qter

A:Introns: 59/3; 85/3; 120/3; 132/3; 143/3; 183/3  
C:Function:  
A:Description: probably helps maintain myelin structure  
C:Superfamily: myelin basic protein  
C:Keywords: acetylated amino end; alternative splicing; citrulline; experimental auto  
F:2-197/Product: myelin basic protein, 21.5K splice form #status predicted <MARI>  
F:2-132,144-197/Product: myelin basic protein, 20.2K splice form #status predicted <MARI>  
F:2-59,86-197/Product: myelin basic protein, 18.5K splice form #status experimental <MARI>  
F:2-59,86-132,144-197/Product: myelin basic protein, 17.2K splice form #status predicted <MARI>  
F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental  
F:26,32,149,157,186,197/Modified site: citrulline (Arg) (in form C-8) #status experimental  
F:134/Modified site: omega-N-methylarginine or omega-N-methylarginine (Arg)  
Query Match 100.0%; Score 260; DB 1; Length 197;  
Best Local Similarity 100.0%; Pred. No. 9,2e-25;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 46  
|||||  
DB 88 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 133  
|||||  
RESULT 2  
MBCZB  
N:Altein basic protein - chimpanzee (tentative sequence)  
N:Alternate names: MBP  
C:Species: Pan troglodytes (chimpanzee)  
C:Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 06-Sep-1996  
C:Accession: A03139  
R:Westall, F.C.; Thompson, M.; Kalter, S.S.  
Life Sci. 17, 219-223, 1975  
A:Title: The proposed sequence of the encephalitogenic protein from chimpanzee brain.  
A:Reference number: A03139; MUID:76009821  
A:Accession: A03139  
A:Molecule type: protein  
A:Residues: 1-171 <MBS>  
C:Comment: This protein may function in maintaining the proper structure of myelin.  
C:Superfamily: myelin basic protein  
C:Keywords: blocked amino end; methylated amino acid; myelin; structural protein  
F:1/Modified site: blocked amino end (Ala) (probably acetylated) #status experimental  
F:107/Modified site: omega-N-methylarginine or omega-N-methylarginine (Arg)  
Query Match 93.1%; Score 242; DB 1; Length 171;  
Best Local Similarity 95.7%; Pred. No. 1.3e-22;  
Matches 44; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 46  
|||||  
DB 61 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 106  
|||||  
RESULT 3  
MBPGB  
N:myelin basic protein - pig (tentative sequence)  
N:Alternate names: myelin Al protein  
N:Contains: myelin basic protein amide 14  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 19-Apr-1996 #sequence\_revision 26-Apr-1996 #text\_change 07-May-1999  
C:Accession: A61640; A36245  
R:Kira, J.; Delbier, G.E.; Kruttsch, H.C.; Martenson, R.E.  
J. Neurochem. 44, 134-142, 1985  
A:Title: Amino acid sequence of porcine myelin basic protein.  
A:Reference number: A61640; MUID:85056964  
A:Accession: A61640  
A:Molecule type: protein  
A:Residues: 1-171 <KIR>  
A:Note: some peptides were ordered by homology  
R:Takamatsu, K.; Tatemoto, K.  
Biochem. Biophys. Res. Commun. 172, 1167-1174, 1990  
A:Title: Isolation and characterization of a novel peptide amide from porcine brain.  
A:Reference number: A36245; MUID:91058553

[illegible]





Best Local Similarity 34.3%; Pred. No. 7.3;  
Matches 12; Conservative 7; Mismatches 16; Indels

Search completed: August 28, 2002, 16:36:03  
Job time: 175 sec

Search completed: August 28, 2002, 16:36:03  
Job time: 175 sec







OM protein - protein search, using sw model

Run on: August 28, 2002, 16:35:33 ; Search time 16.25 seconds  
(without alignments)  
109.606 Million cell updates/sec

Title: US-09-813-383-1  
Perfect score: 260  
Sequence: 1 HHPARTAHYGLPQKSHGRT.....VHFFKNIVTPRTPPSQSGK 46

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	260	100.0	304	1 MBP_HUMAN	P02686 homo sapien
2	242	93.1	171	1 MBP_PANTR	P06906 pan troglod
3	228.5	87.9	171	1 MBP_PIG	P81558 sus scrofa
4	220.5	84.8	169	1 MBP_BOVIN	P02687 bos taurus
5	219.5	84.4	167	1 MBP_CAVPO	P25188 cavia porce
6	218.5	84.0	250	1 MBP_MOUSE	P04370 mus musculu
7	216	83.1	168	1 MBP_RABIT	P25274 oryctolagus
8	204.5	78.7	134	1 MBP_RAT	P02698 rattus norv
9	181.5	69.8	173	1 MBP_CHICK	P15720 gallus gall
10	153	58.8	175	1 MBP_XENLA	P87346 xenopus lae
11	81	31.2	154	1 MBP_RAJER	Q91325 raja erinac
12	81	31.2	154	1 MBP_SQUAC	Q91439 squalus aca
13	80.5	31.0	154	1 MBP_HETFR	P20939 heterodontu
14	65.5	25.2	487	1 OAF_DROME	Q9nla6 drosophila
15	60	23.1	667	1 ENV_GALV	P21415 gibbon ape
16	59.5	22.9	445	1 GDIB_HUMAN	P50395 homo sapien
17	58.5	22.5	405	1 HMX_STRUP	O26656 strongyloce
18	58.5	22.5	445	1 GDIB_CANFA	O97556 canis fami
19	58.5	22.5	445	1 GDIB_MOUSE	P03397 mus musculu
20	57.5	22.1	304	1 HEYL_CANFA	Q9tsz2 canis fami
21	55.5	21.3	218	1 LPOT_MYCLE	Q9cd47 mycobacteri
22	55.5	21.3	679	1 TKT1_YEAST	P23254 saccharomyc
23	55	21.2	555	1 DP87_DICDI	Q04503 dictyosteli
24	54.5	21.0	243	1 NGF_CHICK	P05200 gallus gall
25	54	20.8	238	1 RNPB_HAEIN	P44444 haemophilus
26	54	20.8	640	1 ELM1_YEAST	P32801 saccharomyc
27	53.5	20.6	445	1 GDIC_MOUSE	Q61538 mus musculu
28	53.5	20.6	445	1 GDIC_RAT	P50399 rattus norv
29	53	20.4	231	1 NGF_XENLA	P21617 xenopus lae
30	53	20.4	247	1 Y281_HUMAN	Q92556 homo sapien
31	53	20.4	322	1 REP1_ZYGBI	P13777 zygosacchar
32	53	20.4	329	1 TECB_CHICK	P54097 gallus gall
33	52.5	20.2	202	1 VIC2_AGR6	P06666 agrobacteri

34	52.5	20.2	2128	1 SPCB_MOUSE	P15508 mus musculu
35	52.5	20.2	2137	1 SPCB_HUMAN	P11277 homo sapien
36	52	20.0	376	1 FXL2_HUMAN	P58012 homo sapien
37	52	20.0	479	1 YP66_YEAST	Q12194 saccharomyc
38	52	20.0	677	1 SGL_HUMAN	P05060 homo sapien
39	52	20.0	1053	1 FAK1_CHICK	Q00944 gallus gall
40	52	20.0	2300	1 CYAA_NEUCR	Q01631 neurospora
41	51.5	19.8	273	1 DLX3_NOTVI	P53770 notophthalm
42	51.5	19.8	1108	1 DBS_HUMAN	O15068 homo sapien
43	51.5	19.8	1149	1 DBS_MOUSE	Q64096 mus musculu
44	51.5	19.8	1736	1 ZOI_HUMAN	Q07157 homo sapien
45	51	19.6	523	1 TP6B_METTH	O27088 methanobact

## ALIGNMENTS

RESULT 1	
MBP_HUMAN	
ID	MBP_HUMAN STANDARD; PRT; 304 AA.
AC	P02686; Q15337; Q15338; Q15339; Q15340;
DT	21-JUL-1986 (Rel. 01, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	01-MAR-2002 (Rel. 41, Last annotation update)
DE	Myelin basic protein (MBP) (Myelin A1 protein) (Myelin membrane encephallitogenic protein).
GN	MBP.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC	TISSUE=Brain;
RX	MEDLINE=94068468; PubMed=7504278;
RA	Pribyl T.M., Campagnoni C.W., Kampf K., Kashima T., Handley V.W., McMahon J., Campagnoni A.T.;
RT	"The myelin basic protein gene is included within a 179-kilobase transcripition unit; expression in the immune and central nervous systems."
RT	Proc. Natl. Acad. Sci. U.S.A. 90:10695-10699(1993).
RL	[2]
RP	SEQUENCE FROM N.A. (ISOFORMS 3; 4; 5 AND 6).
RC	TISSUE=Embryonic spinal cord;
RX	MEDLINE=87311781; PubMed=2442403;
RA	Roth H.J., Kronquist K.E., de Rosbo N., Crandall B.F., Campagnoni A.T.;
RT	"Evidence for the expression of four myelin basic protein variants in the developing human spinal cord through cDNA cloning."
RT	J. Neurosci. Res. 17:321-328(1987).
RL	[3]
RP	SEQUENCE FROM N.A. (ISOFORM 6).
RC	TISSUE=Embryonic spinal cord;
RX	MEDLINE=86308101; PubMed=2427738;
RA	Roth H.J., Kronquist K.E., Pretorius P.J., Crandall B.F., Campagnoni A.T.;
RT	"Isolation and characterization of a cDNA coding for a novel human 17.3K myelin basic protein (MBP) variant."
RT	J. Neurosci. Res. 16:227-238(1986).
RL	[4]
RP	SEQUENCE FROM N.A. (ISOFORMS 3 AND 5).
RC	MEDLINE=86259714; PubMed=2425357;
RA	Kamholz J., de Ferra F., Puckett C., Lazzarini R.A.;
RT	"Identification of three forms of human myelin basic protein by cDNA cloning."
RT	Proc. Natl. Acad. Sci. U.S.A. 83:4962-4966(1986).
RL	[5]
RP	SEQUENCE FROM N.A. (ISOFORMS 3; 4; 5 AND 6).
RC	MEDLINE=89302693; PubMed=2472816;
RA	Streicher R., Stoffel W.;
RT	"The organization of the human myelin basic protein gene. Comparison with the mouse gene."
RT	Biol. Chem. Hoppe-Seyler 370:503-510(1989).

RN [6] SEQUENCE FROM N.A. (ISOFORM 5).  
 RC TISSUE=Melanoma;  
 RA Strausberg R.;  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE (ISOFORM 5).  
 RX MEDLINE=72066400; PubMed=4108501;  
 RA Carnegie P.R.;  
 RT "Amino acid sequence of the encephalitogenic basic protein from human  
 myelin.";  
 RL Biochem. J. 123:57-67(1971).  
 RN [8]  
 RP SEQUENCE OF 135-192 FROM N.A.  
 RX MEDLINE=90152679; PubMed=1689270;  
 RA Boylan K.B., Ayres T.M., Popko B., Takahashi N., Hood L.E.,  
 Prusiner S.B.;  
 RT "Repetitive DNA (TGGA)n 5' to the human myelin basic protein gene: a  
 new form of oligonucleotide repetitive sequence showing length  
 polymorphism.";  
 RL Genomics 6:16-22(1990).  
 RN [9]  
 RP SEQUENCE OF 179-222 (ISOFORM 5), AND REVISIONS.  
 RA Shapira R., McKeally S.S., Chou F., Kibler R.F.;  
 RT "Encephalitogenic fragment of myelin basic protein. Amino acid  
 sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";  
 RL J. Biol. Chem. 246:4630-4640(1971).  
 RN [10]  
 RP SEQUENCE OF 135-178 AND 224-304 (ISOFORM 3), AND MASS SPECTROMETRY.  
 RX MEDLINE=86280476; PubMed=2426402;  
 RA Scoble H.A., Whitaker J.N., Biemann K.;  
 RT "Analysis of the primary sequence of human myelin basic protein  
 peptides 1-44 and 90-170 by fast atom bombardment mass spectrometry.";  
 RL J. Neurochem. 47:614-616(1986).  
 RN [11]  
 RP SEQUENCE OF 148-304 (ISOFORM 5), AND CITRULLINATION OF C8.  
 RC TISSUE=Brain;  
 RX MEDLINE=89174797; PubMed=2466844;  
 RA Wood D.D., Moscarello M.A.;  
 RT "The isolation, characterization, and lipid-aggregating properties of  
 a citrulline containing myelin basic protein.";  
 RL J. Biol. Chem. 264:5121-5127(1989).  
 RN [12]  
 RP SEQUENCE OF 179-223 (ISOFORM 5), AND MASS SPECTROMETRY.  
 RX MEDLINE=84185608; PubMed=6201481;  
 RA Gibson B.W., Gilliom R.D., Whitaker J.N., Biemann K.;  
 RT "Amino acid sequence of human myelin basic protein peptide 45-89 as  
 determined by mass spectrometry.";  
 RL J. Biol. Chem. 259:5028-5031(1984).  
 RN [13]  
 RP SEQUENCE OF 246-269 (ISOFORM 3), AND ENCEPHALITOGENTIC PEPTIDE.  
 RX MEDLINE=71088405; PubMed=4099524;  
 RA Lennon V.A., Wilks A.V., Carnegie P.R.;  
 RT "Immunologic properties of the main encephalitogenic peptide from the  
 basic protein of human myelin.";  
 RL J. Immunol. 105:1223-1230(1970).  
 RN [14]  
 RP SEQUENCE OF 156-172 AND 302-304, AND CHARACTERIZATION OF C8.  
 RC TISSUE=Brain;  
 RX MEDLINE=96004793; PubMed=7574672;  
 RA Boulias C., Pang H., Mastronardi F., Moscarello M.A.;  
 RT "The isolation and characterization of four myelin basic proteins from  
 the unbound fraction during CM52 chromatography.";  
 RL Arch. Biochem. Biophys. 322:174-182(1995).  
 RN [15]  
 RP METHYLATION  
 RX MEDLINE=72066401; PubMed=5128665;  
 RA Baldwin G.S., Carnegie P.R.;  
 RT "Isolation and partial characterization of methylated arginines from  
 the encephalitogenic basic protein of myelin.";  
 RL Biochem. J. 123:69-74(1971).  
 RN [16]  
 RP STRUCTURE OF 135-148 BY NMR.  
 RX MEDLINE=95377296; PubMed=7544282;  
 RA Mendz G.L., Barden J.A., Martenson R.E.;  
 RT "Conformation of a tetradecapeptide epitope of myelin basic protein.";  
 RL Eur. J. Biochem. 231:659-666(1995).  
 RN [17]  
 RP 3D-STRUCTURE MODELING OF 135-279 (ISOFORM 5).  
 RX MEDLINE=97172499; PubMed=9020143;  
 RA Ridsdale R.A., Beniac D.R., Tompkins T.A., Moscarello M.A., Harauz G.;  
 RT "Three-dimensional structure of myelin basic protein. II. Molecular  
 modeling and considerations of predicted structures in multiple  
 sclerosis.";  
 RL J. Biol. Chem. 272:4269-4275(1997).  
 RN [18]  
 RP FUNCTION: The classic group of MBP isoforms (isoforms 4-14) are  
 with PLP the most abundant protein components of the myelin  
 membrane in the CNS. They have a role in both its formation and  
 stabilization. The smaller isoforms might have an important role  
 in remyelination of denuded axons in multiple sclerosis. The non-  
 classic group of MBP isoforms (isoforms 1-3/Golli-MBPs) may  
 preferentially have a role in the early developing brain long  
 before myelination, maybe as components of transcriptional  
 complexes, and may also be involved in signaling pathways in T-  
 cells and neural cells. Differential splicing events combined to  
 optional posttranslational modifications give a wide spectrum of  
 isoforms, each of them having maybe a specialized function.  
 CC -! SUBUNIT: Homodimer (By similarity).  
 CC -! SUBCELLULAR LOCATION: Cytoplasmic side of myelin.  
 CC -! ALTERNATIVE PRODUCTS: At least 6 isoforms: 1/Golli-MBP1/HOG7  
 5/MBP3, 2/Golli-MBP2/HOG5, 3/MBP1/21.5 kDa, 4/MBP2/20.2 kDa,  
 6/MBP4/17.2 kDa; are produced by alternative  
 splicing.  
 CC -! TISSUE SPECIFICITY: MBP isoforms are found in both the central and  
 the peripheral nervous system, whereas Golli-MBP isoforms are  
 expressed in fetal thymus, spleen and spinal cord, as well as in  
 cell lines derived from the immune system.  
 CC -! DEVELOPMENTAL STAGE: Expression turns on abruptly in fetus of 14  
 to 16 weeks. Even smaller isoforms seem to be produced during  
 embryogenesis, some of these persisting in the adult. Expression  
 of MBP is more evident at 16 weeks and its relative  
 proportion declined thereafter.  
 CC -! PTM: Several charge isomers of MBP: C1 (the most cationic, least  
 modified, and most abundant form), C2, C3, C4, C5, C6, C7, C8-A  
 and C8-B (the less cationic form); are produced as a result of  
 optional PTM, such as phosphorylation, deamidation of glutamine or  
 asparagine, arginine citrullination and methylation. C8-A and C8-B  
 contain each two mass isoforms termed C8-A(H), C8-A(L), C8-B(H)  
 and C8-B(L), (H) standing for higher and (L) for lower molecular  
 weight. C3, C4 and C5 are phosphorylated. The ratio of methylated  
 arginine residues decreases in aging, making the protein more  
 cationic.  
 CC -! DISEASE: The reduction in the surface charge of citrullinated  
 and/or methylated MBP could result in a weakened attachment to the  
 myelin membrane. This mechanism could be operative in  
 demyelinating diseases such as chronic multiple sclerosis (MS),  
 and fulminating MS (Marburg's disease).  
 CC -! SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed, usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; L18866; AAA72011.1; -;  
 DR EMBL; L18865; AAA72010.1; -;  
 DR EMBL; L18864; AAA72009.1; -;  
 DR EMBL; L18862; AAA72008.1; -;  
 DR EMBL; M30516; AAA59563.1; -;  
 DR EMBL; M30515; AAA59564.1; -;  
 DR EMBL; M30047; AAA59559.1; -;  
 DR EMBL; M33577; AAA59562.1; -;  
 DR EMBL; M20009; AAA59561.1; -;  
 DR

Query Match 100.0%; Score 260; DB 1; Length 304;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-25;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYSLPQKSHGRTOENPVVHFKNIVTPTPTPPSQGK 46  
 DB 195 HHPARTAHYSLPQKSHGRTOENPVVHFKNIVTPTPTPPSQGK 240

## RESULT 2

MBP\_PANTR MBP\_PANTR STANDARD; PRT; 171 AA.  
 AC P06906;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Myelin basic protein (MBP).  
 GN MBP.  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 OX NCBI\_TaxID=9598;  
 RN [1]  
 RP PRELIMINARY SEQUENCE.  
 RX MEDLINE=76009821; PubMed=51459;  
 RA Westall F.C., Thompson M., Kaiter S.S.;  
 RT "The proposed sequence of the encephalitogenic protein from  
 chimpanzee brain.";  
 RL Life Sci. 17:219-223(1975).  
 CC -1- FUNCTION: Is, with PLP, the most abundant protein component of the  
 myelin membrane in the CNS. Has a role in both the formation and  
 stabilization of this compact multilayer arrangement of bilayers.  
 CC Each splice variant and charge isomer may have a specialized  
 function in the assembly of an optimized, biochemically functional  
 myelin membrane (By similarity).  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.  
 CC -1- PTM: As in other animals, several charge isomers may be produced  
 as a result of optional posttranslational modifications, such as  
 phosphorylation of serine or threonine residues, deamidation of  
 glutamine or asparagine residues, citrullination and methylation  
 of arginine residues.  
 CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.  
 DR PIR; A03139; MRC2B.  
 DR HSP; P02686; IQCL.  
 DR InterPro; IPR000548; Myelin\_BP.  
 DR Pfam; PF01669; Myelin\_MBP; 1.  
 DR PRINTS; PR00212; MYELINMBP.  
 DR PROSITE; PS00569; MYELIN\_MBP; 1.  
 KW Myelin; Structural protein; Acetylation; Methylation; Phosphorylation;  
 Citrullination; Autoimmune encephalomyelitis.  
 FT MOD\_RES 1 1 ACETYLATION.  
 FT MOD\_RES 7 7 PHOSPHORYLATION (PARTIAL) (BY  
 SIMILARITY).  
 FT MOD\_RES 25 25 CITRULLINATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 31 31 CITRULLINATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 56 56 PHOSPHORYLATION (PARTIAL) (BY  
 SIMILARITY).  
 FT MOD\_RES 98 98 PHOSPHORYLATION (PARTIAL) (BY  
 SIMILARITY).  
 FT MOD\_RES 103 103 DEAMIDATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 107 107 METHYLATION (MONO-OR DI-) (BY  
 SIMILARITY).  
 FT MOD\_RES 115 115 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 122 122 CITRULLINATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 130 130 CITRULLINATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 148 148 DEAMIDATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 160 160 CITRULLINATION (PARTIAL) (BY  
 SIMILARITY).  
 FT MOD\_RES 162 162 PHOSPHORYLATION (PARTIAL) (BY  
 SIMILARITY).  
 FT MOD\_RES 166 166 PHOSPHORYLATION (PARTIAL) (BY  
 SIMILARITY).

FT MOD\_RES 171 171 CITRULLINATION (BY SIMILARITY).  
 SQ SEQUENCE 171 AA; 18560 MW; 59FED59DE6933293 CRC64;

Query Match 93.1%; Score 242; DB 1; Length 171;  
 Best Local Similarity 95.7%; Pred. No. 2.4e-23;  
 Matches 44; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HHPARTAHYSLPQKSHGRTOENPVVHFKNIVTPTPTPPSQGK 46  
 DB 61 HHPARTAHYSLPQKSHGRTOENPVVHFKNIVTPTPTPPSQGK 106

## RESULT 3

MBP\_PIG MBP\_PIG STANDARD; PRT; 171 AA.  
 ID P81558; P98189;  
 AC P81558; P98189; (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Myelin basic protein (MBP).  
 GN MBP.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE, AND METHYLATION OF ARG-107.  
 RC TISSUE=Brain;  
 RX MEDLINE=85056964; PubMed=2578056;  
 RA Kira J.-I., Deibler G.E., Krutzsch H.C., Martenson R.E.;  
 RT "Amino acid sequence of porcine myelin basic protein.";  
 RL J. Neurochem. 44:134-142(1985).  
 CC [2]  
 RN ERRATUM.  
 RA Kira J.-I., Deibler G.E., Krutzsch H.C., Martenson R.E.;  
 RL J. Neurochem. 44:1663-1663(1985).  
 CC -1- FUNCTION: Is, with PLP, the most abundant protein component of the  
 myelin membrane in the CNS. Has a role in both the formation and  
 stabilization of this compact multilayer arrangement of bilayers.  
 CC Each splice variant and charge isomer may have a specialized  
 function in the assembly of an optimized, biochemically functional  
 myelin membrane (By similarity).  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.  
 CC -1- PTM: As in other animals, several charge isomers may be produced  
 as a result of optional posttranslational modifications, such as  
 phosphorylation of serine or threonine residues, deamidation of  
 glutamine or asparagine residues, citrullination and methylation  
 of arginine residues.  
 CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.  
 DR HSP; P02686; IQCL.  
 DR InterPro; IPR000548; Myelin\_BP.  
 DR Pfam; PF01669; Myelin\_MBP; 1.  
 DR PRINTS; PR00212; MYELINMBP.  
 DR PROSITE; PS00569; MYELIN\_MBP; 1.  
 KW Myelin; Structural protein; Acetylation; Methylation; Phosphorylation;  
 Citrullination.  
 FT MOD\_RES 1 1 ACETYLATION.  
 FT MOD\_RES 7 7 PHOSPHORYLATION (PARTIAL) (BY  
 SIMILARITY).  
 FT MOD\_RES 25 25 CITRULLINATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 31 31 CITRULLINATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 55 55 PHOSPHORYLATION (PARTIAL) (BY  
 SIMILARITY).  
 FT MOD\_RES 98 98 PHOSPHORYLATION (PARTIAL) (BY  
 SIMILARITY).  
 FT MOD\_RES 103 103 DEAMIDATION (MONO-OR DI-).  
 FT MOD\_RES 107 107 METHYLATION (BY SIMILARITY).  
 FT MOD\_RES 115 115 PHOSPHORYLATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 130 130 CITRULLINATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 148 148 DEAMIDATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 160 160 CITRULLINATION (PARTIAL) (BY SIMILARITY).





DB 61 HHAARTHYGSLPKSQ-RSQDENPVVHFKNIVTPTPPPSOGK 105

RESULT 6

MBP\_MOUSE

ID MBP\_MOUSE STANDARD; PRT: 250 AA.

AC P04370; Q03139; Q01585; Q03176; Q09WPL; Q99KE4; Q61836; Q61837;

DT 20-MAR-1987 (Rel. 04, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Myelin basic protein (MBP) (Myelin A1 protein).

OS MBP OR SHI

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_Taxid=10090;

[1]

RN SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).

RC STRAIN=C57BL/6; TISSUE=Brain;

RX MEDLINE=93186801; PubMed=7680345;

RA Campagnoni A.T., Pribyl T.M., Campagnoni C.W., Kampf K.,

RA Anur-Umarjee S., Landry C.F., Handley V.W., Newman S., Garbay B.,

RA Kitamura K.;

RT "Structure and developmental regulation of Golli-mbp, a 105-kilobase

RT gene that encompasses the myelin basic protein gene and is expressed

RT in cells in the oligodendrocyte lineage in the brain.";

RL J. Biol. Chem. 268:4930-4938(1993).

[2]

RN SEQUENCE FROM N.A. (ISOFORM 2).

RC STRAIN=C57BL/6; TISSUE=Bone marrow;

RX MEDLINE=93057537; PubMed=1279125;

RA Grima B., Zelenika D., Pessac B.;

RT "A novel transcript overlapping the myelin basic protein gene.";

RL J. Neurochem. 59:2318-2323(1992).

[3]

RN SEQUENCE FROM N.A. (ISOFORMS 4; 5; 6 AND 8).

RX MEDLINE=86079555; PubMed=2416470;

RA de Ferreira F., Engh H., Hudson L., Kamholz J., Puckett C., Molineux S.,

RA Lazzarini R.A.;

RT "Alternative splicing accounts for the four forms of myelin basic

RT protein.";

RL Cell 43:721-727(1985).

[4]

RN SEQUENCE FROM N.A. (ISOFORM 5).

RX MEDLINE=85254913; PubMed=2410136;

RA Takahashi N., Roach A., Teplow D.B., Prusiner S.B., Hood L.E.;

RT "Cloning and characterization of the myelin basic protein gene from

RT mouse: one gene can encode both 14 kd and 18.5 kd MBPs by alternate

RT use of exons.";

RL Cell 42:139-148(1985).

[5]

RN SEQUENCE FROM N.A. (ISOFORM 6), AND SEQUENCE OF 9-194 FROM N.A.

RP (ISOFORM 7).

RC STRAIN=C57BL/6J; TISSUE=Brain;

RX MEDLINE=87118269; PubMed=2433693;

RA Newman S., Kitamura K., Campagnoni A.T.;

RT "Identification of a cDNA coding for a fifth form of myelin basic

RT protein in mouse.";

RL Proc. Natl. Acad. Sci. U.S.A. 84:886-890(1987).

[6]

RN SEQUENCE FROM N.A. (ISOFORM 8).

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

[7]

RN SEQUENCE FROM N.A. (ISOFORM 9).

RC TISSUE=Breast tumor;

RA Strausberg R.;

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

[8]

RN SEQUENCE OF 135-157 FROM N.A.

EX MEDLINE=89252919; PubMed=2470651;

RA Miura M., Tamura T.A., Aoyama A., Mikoshiba K.;

RT "The promoter elements of the mouse myelin basic protein gene

RT function efficiently in NG108-15 neuronal/gial cells.";

RL Gene 75:31-38(1989).

[9]

RN PARTIAL SEQUENCE FROM N.A. (25 AA INSERTION OF ISOFORMS 4; 6 AND 9).

EX MEDLINE=86259714; PubMed=2425357;

RA Kamholz J., de Ferreira F., Puckett C., Lazzarini R.A.;

RT "Identification of three forms of human myelin basic protein by cDNA

RT cloning.";

RL Proc. Natl. Acad. Sci. U.S.A. 83:4962-4966(1986).

[10]

RN SEQUENCE OF 193-222 FROM N.A.

EX MEDLINE=84119431; PubMed=6198644;

RA Zeller N.K., Hunkeler M.J., Campagnoni A.T., Sprague J.,

RA Lazzarini R.A.;

RT "Characterization of mouse myelin basic protein messenger RNAs with a

RT myelin basic protein cDNA clone.";

RL Proc. Natl. Acad. Sci. U.S.A. 81:18-22(1984).

[11]

RN PARTIAL SEQUENCE FROM N.A. (22 AA INSERTION OF ISOFORMS 10 AND 11).

RC TISSUE=Spinal cord;

RX MEDLINE=91162193; PubMed=1705957;

RA Aruga J., Okano H., Mikoshiba K.;

RT "Identification of the new isoforms of mouse myelin basic protein: the

RT existence of exon 5a.";

RL J. Neurochem. 56:1222-1226(1991).

[12]

RN PARTIAL SEQUENCE FROM N.A. (ISOFORMS 12; 13 AND 14).

EX MEDLINE=93203893; PubMed=7681106;

RA Nakajima K., Ikenaka K., Kagawa T., Aruga J., Nakao J., Nakahira K.,

RA Shiota C., Kim S.U., Mikoshiba K.;

RT "Novel isoforms of mouse myelin basic protein predominantly expressed

RT in embryonic stage.";

RL J. Neurochem. 60:1554-1563(1993).

[13]

RN SEQUENCE OF 191-224 FROM N.A.

EX MEDLINE=88196094; PubMed=2452084;

RA Okano H., Tamura T., Miura M., Aoyama A., Ikenaka K., Oshimura M.,

RA Mikoshiba K.;

RT "Gene organization and transcription of duplicated MBP genes of myelin

RT deficient (shi<sup>mld</sup>) mutant mouse.";

RL EMBO J. 7:77-83(1988).

[14]

RN DEVELOPMENTAL STAGE.

RX MEDLINE=98409779; PubMed=9736652;

RA Landry C.F., Pribyl T.M., Ellison J.A., Givogri M.I., Kampf K.,

RA Campagnoni C.W., Campagnoni A.T.;

RT "Embryonic expression of the myelin basic protein gene: identification

RT of a promoter region that targets transgene expression to pioneer

RT neurons.";

RL J. Neurosci. 18:7315-7327(1998).

[15]

RN FUNCTION.

RX MEDLINE=21018209; PubMed=11145205;







```

RESULT 9
MBP_CHICK
ID MBP_CHICK STANDARD; PRT; 173 AA.
AC P15720;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Myelin basic protein (MBP).
GN MBP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=White leghorn; TISSUE=Optic lobe;
RA MEDLINE=89358239; PubMed=2475444;
RX Zopf D., Sonntag H., Betz H., Gundelfinger E.D.;
RT "Developmental accumulation and heterogeneity of myelin basic protein
transcripts in the chick visual system.";
RL Glia 2:241-249(1989).
CC -1- FUNCTION: Is, with PLP, the most abundant protein component of the
myelin membrane in the CNS. Has a role in both the formation and
stabilization of this compact multilayer arrangement of bilayers.
CC Each splice variant and charge isomer may have a specialized
function in the assembly of an optimized, biochemically functional
myelin membrane (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
CC here) and 2: are produced by alternative splicing.
CC -1- ALTERNATIVE PRODUCTS: At least 2 isoforms: 1 (major form) (shown
here) and 2: are produced by alternative splicing.
CC -1- DEVELOPMENTAL STAGE: In the optic lobe, first detected at
embryonic day 14. Expression strongly increases between day 1, and then
declines again to the adult level.
CC -1- PTM: As in other animals, several charge isomers may be produced
as a result of optional posttranslational modifications, such as
phosphorylation of serine or threonine residues, deamidation of
glutamine or asparagine residues, citrullination and methylation
of arginine residues.
CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X17103; CA34959.1; -
DR PIR; S08535; S08535.
DR HSP; P02686; LOCL.
DR InterPro; IPR000548; Myelin_BP.
DR Pfam; PF01669; Myelin_MBP; 1.
DR PRINTS; PR00212; MYELINMBP.
DR PROSITE; PS00569; MYELIN_MBP; 1.
KW Myelin; Structural protein; Acetylation; Methylation; Phosphorylation;
KW Citrullination; Alternative splicing.
FT INIT_MET 0 0 BY SIMILARITY.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT MOD_RES 7 7 PHOSPHORYLATION (PARTIAL) (BY
FT SIMILARITY).
FT MOD_RES 24 24 CITRULLINATION (PARTIAL) (BY SIMILARITY).
FT MOD_RES 29 29 CITRULLINATION (PARTIAL) (BY SIMILARITY).
FT MOD_RES 96 96 PHOSPHORYLATION (PARTIAL) (BY
FT SIMILARITY).
FT MOD_RES 101 101 DEAMIDATION (PARTIAL) (BY SIMILARITY).
FT MOD_RES 105 105 METHYLATION (MONO-OR DI-) (BY
FT SIMILARITY).
FT MOD_RES 113 113 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 146 146 DEAMIDATION (PARTIAL) (BY SIMILARITY).

Query Match 69.8%; Score 181.5; DB 1; Length 173;
Best Local Similarity 71.7%; Pred. No. 8.7e-16;
Matches 33; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

OY 2 HPARTAHYGLSPQKS-HGRTQDENPVVHFKNIVTRTPPPSQGKG 46
| | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 59 HAARASHVGSIPQSRQGRGDDNPVHFKNIVSPRTPPPMQAKG 104
| | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 10
MBP_XENLA
ID MBP_XENLA STANDARD; PRT; 175 AA.
AC P87346;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myelin basic protein (MBP) (Myelin A1 protein).
GN MBP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J; TISSUE=Brain;
RA Nagata S., Ogino K.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Is, with PLP, the most abundant protein component of the
myelin membrane in the CNS. Have a role in both the formation and
stabilization of this compact multilayer arrangement of bilayers.
CC Each splice variant and charge isomer may have a specialized
function in the assembly of an optimized, biochemically functional
myelin membrane (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
CC -1- PTM: As in other animals, several charge isomers may be produced
as a result of optional posttranslational modifications, such as
phosphorylation of serine or threonine residues, deamidation of
glutamine or asparagine residues, citrullination and methylation
of arginine residues.
CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB000736; BAAL19174.1; -
DR HSP; P02686; LOCL.
DR InterPro; IPR000548; Myelin_BP.
DR Pfam; PF01669; Myelin_MBP; 1.
DR PRINTS; PR00212; MYELINMBP.
KW Myelin; Structural protein; Acetylation; Methylation; Phosphorylation;
KW Citrullination.
FT INIT_MET 0 0 BY SIMILARITY.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT MOD_RES 6 6 PHOSPHORYLATION (PARTIAL) (BY
FT SIMILARITY).
FT MOD_RES 24 24 CITRULLINATION (PARTIAL) (BY SIMILARITY).
FT MOD_RES 32 32 CITRULLINATION (PARTIAL) (BY SIMILARITY).

```

CC	EMBL; U44053; AAA96756.1; -	BY SIMILARITY.
DR	HSP; P02686; IQCL	0
DR	InterPro: IPR000548; Myelin_BP.	1
DR	Pfam: PF01669; Myelin_MBP; 1.	30
DR	PRINTS; PR00212; MYELINMBP.	30
DR	PROSITE; PS00569; MYELIN_MBP; 1.	30
DR	Protein; Structural protein; Acetylation; Phosphorylation.	30
DR	INIT_MET	0
FT	MOD_RES	1
FT	VARIANT	30
FT	VARIANT	30
FT	VARIANT	30
FT	SEQUENCE	154 AA; 16451 MW; 30A0ED482B4BA681 CRC64;

RESULT	ID	MBP_HETFR	STANDARD	PRT	154 AA.
13	MBP_HETFR	AC	P20939;		
	DT	01-FEB-1991	(Rel. 17, Created)		
	DT	01-FEB-1991	(Rel. 17, Last sequence update)		
	DT	30-MAY-2000	(Rel. 39, Last annotation update)		





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OM protein - protein search, using sw model

Run on: August 28, 2002, 16:35:08 ; Search time 41.39 Seconds  
(without alignments)  
192.263 Million cell updates/sec

Title: US-09-813-383-1

Perfect score: 260

Sequence: 1 HHPARTAHYGLPQKSHGRT.....VHFFKNIVTPPPPSQGK 46

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL19.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_virus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaea.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78.5	30.2	128	13	P98190 carcharhinu
2	64.5	24.8	448	13	O93382 gallus gall
3	63	24.2	632	16	O91250 pseudomonas
4	62	23.8	709	5	O9VU89 drosophila
5	60.5	23.3	1723	4	O92576 homo sapien
6	60.5	23.3	1957	4	O92576 homo sapien
7	60.5	23.3	2039	4	O9U145 homo sapien
8	60	23.1	676	5	O95WV0 drosophila
9	60	23.1	685	15	O9YWM3 gibbon ape
10	59.5	22.9	2556	11	O91XW2 mus musculus
11	59	22.7	238	2	O9AES0 pasteurilla
12	59	22.7	248	10	O9ASD4 oryza sativ
13	59	22.7	401	5	O965J5 caenorhabdi
14	59	22.7	441	5	O27378 caenorhabdi
15	59	22.7	556	16	O9JVG1 neisseria m
16	59	22.7	608	16	O9K0G2 neisseria m

17	59	22.7	625	2	O9R9E7
18	59	22.7	736	10	O23362
19	59	22.7	1160	12	O86928
20	59	22.7	1514	4	O9H0B0
21	59	22.7	1564	4	O96JN8
22	58.5	22.5	567	5	O9V925
23	58.5	22.5	607	5	O960E4
24	57.5	22.1	266	12	O56868
25	57	21.9	137	6	O9BDE4
26	56.5	21.7	363	16	O9AQQ7
27	56.5	21.7	444	11	O62219
28	56.5	21.7	462	12	O40938
29	56.5	21.7	760	13	O9DDU6
30	56.5	21.7	2228	10	O48579
31	56	21.5	235	2	O9X528
32	56	21.5	562	5	O22068
33	56	21.5	564	5	O952Q4
34	56	21.5	576	10	O9L0F5
35	55.5	21.3	943	5	O9VF63
36	55.5	21.3	973	4	O9P203
37	55	21.2	257	16	O9KVD6
38	55	21.2	262	4	O9UJ34
39	55	21.2	422	10	O23764
40	55	21.2	579	4	O9H7K3
41	55	21.2	732	5	O960C3
42	55	21.2	891	16	O9PAG7
43	55	21.2	1016	4	O9BR83
44	55	21.2	1184	4	O9BS08
45	55	21.2	1751	5	O17143

## ALIGNMENTS

RESULT 1

P98190	ID	P98190	PRELIMINARY;	PRT;	128 AA.
AC	P98190;				
DT	01-MAY-2000	(TrEMBLrel. 13, Created)			
DT	01-MAY-2000	(TrEMBLrel. 13, Last sequence update)			
DT	01-JUN-2001	(TrEMBLrel. 17, Last annotation update)			
DE	MYELIN BASIC PROTEIN (MBP) (FRAGMENTS).				
OS	Carcharias obscurus (Dusky shark).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;				
OC	Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;				
OC	Carcharhinidae; Carcharhinus.				
OX	NCBI_TaxID=7807;				
RN	[1]				
RP	SEQUENCE.				
RC	TISSUE-BRAIN;				
RX	MEDLINE-90347482; PubMed-1696624;				
RA	Milne T.J., Atkins A.R., Warren J.A., Auton W.P., Smith R.;				
RT	"Shark myelin basic protein: amino acid sequence, secondary structure, and self-association.";				
RT	J. Neurochem. 55:950-955(1990).				
RL	- FUNCTION: CONSTITUTES WITH LIPOPHILLIN THE MAJOR PROTEINS OF MYELIN IN THE CNS (85% OF THE TOTAL MEMBRANE PROTEINS). ASSOCIATES PRIMARILY WITH ACIDIC LIPIDS, FLUIDIZES THE BILAYER AND ALTERS ITS PERMEABILITY. INDUCES THE FORMATION OF A COMPACT MULTILAYER ARRANGEMENT OF BILAYERS (BY SIMILARITY).				
CC	- SUBUNIT: SELF-ASSOCIATES IN THE PRESENCE OF LYSOLIPID (BY SIMILARITY).				
CC	- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.				
CC	- PTM: THE N-TERMINUS IS BLOCKED (PROBABLE).				
DR	HSP: P02686; LOC.				
DR	InterPro: IPR000548; Myelin_BP.				
DR	Pfam: PF01669; Myelin_MBP; 1.				
DR	PROSITE: PS00569; MYELIN_MBP; 1.				
KW	Myelin; Structural protein; Phosphorylation.				
FT	NON_TER 1 1				
FT	NON_CONS 5 6				
FT	MOD_RES 55 55				
FT	MOD_RES 65 65				
FT	DEAMIDATION (PARTIAL) (BY SIMILARITY).				
FT	DEAMIDATION (PARTIAL) (BY SIMILARITY).				

O9R9E7	pseudomonas
O23362	arabidopsis
O86928	parvo-like
O9H0B0	homo sapien
O96JN8	homo sapien
O9V925	drosophila
O960E4	drosophila
O56868	gallid herp
O9BDE4	bos taurus
O9AQQ7	streptococ
O62219	mus musculu
O40938	kaposi's sa
O9DDU6	xenopus lae
O48579	arabidopsis
O9X528	legionella
O22068	caenorhabdi
O952Q4	caenorhabdi
O9L0F5	arabidopsis
O9VF63	drosophila
O9P203	homo sapien
O9KVD6	homo sapien
O9UJ34	homo sapien
O23764	craterostig
O9H7K3	homo sapien
O960C3	drosophila
O9PAG7	xytella fas
O9BR83	homo sapien
O9BS08	homo sapien
O17143	drosophila

FT	MOD_RES	124	124		PHOSPHORYLATION (PARTIAL) (BY SIMILARITY).
FT	MOD_RES	128	128		CITRULLINATION (BY SIMILARITY).
SQ	SEQUENCE	128 AA;	13747 MW;	104E952B79A4D79 CRC64;	
 Query Match            30, 28;    Score 78.5;    DB 13;    Length 128; Best Local Similarity   43.68;   Pred. No. 0.0083; Matches 17;    Conservative 7;   Mismatches 6;   Indels     9;   Gaps					
OY	4	ARTAHVGSLPQKSH---CRTGDENPVVHFFKNIVTPRP 39			
Db	30	APTLH-----KAHQAGRTDDSAVVHFFKNMSPRAP 62			
 RESULT        2					
ID	O93382	PRELIMINARY;	PRT:	448 AA.	
AC	O93382;				
Dt	01-NOV-1998	(TReMBLrel. 08, Created)			
DT	01-NOV-1998	(TReMBLrel. 08, Last sequence update)			
DE	01-DEC-2001	(TReMBLrel. 19, Last annotation update)			
DE	RAB-GDP DISSOCIATION INHIBITOR.				
OS	Gallus gallus	(Chicken).			
OC	Eukaryota;	Metazoa;	Chordata;	Craniata;	Vertebrata;
OC	Archosauria;	Aves;	Neognathae;	Galliformes;	Phasianidae;
OX	Gallus				
NCBI_TaxID=9031;					
[1]					
RP	SEQUENCE FROM N.A.				
RN	TISSUE=CILIARY GLANDLIGN;				
RC	MEDLINE=98363727; PubMed=9698324;				
RA	Inokomov O.C., Kulesa M.C., Shisheva A.C., Jacob M.H.;				
RT	"Innervation and target tissue interactions induce Rab-GDP				
RT	dissociation inhibitor (GDI) expression during peripheral synapse				
RL	formation in developing chick ciliary ganglion neurons [in situ]."				
J. Neurosci.	18:6331-6339(1998).				
EMBL;	AF076291; AAC31910.1; -.				
HSSP;	P21856; LGND.				
InterPro:	IPR002005; Rab_GDI_REP.				
Pfam;	PF00996; GDI; 1.				
PRINTS;	PRO0891; RABGDIREP.				
SEQUENCE	448 AA; 50683 MW;				
87F93A96CD51F83 CRC64.					

Query Match 24.8%; Score 64.5; DB 13; Length 448;  
Best Local Similarity 31.1%; Pred. No. 2.4;  
Matches 14; Conservative 6; Mismatches 18; Indels 7; Gaps 1;

**QY** 2 HPARTAHYGSLPQKSHCRTODENPVVHFKNIVPTPTPPSQKG 46  
| | : : || | : | : | | | | : |  
**Db** 32 HMDRNSYVG-----GESATIPLEDLYKRNLPGTPPSMGRG 69

RESULT 3  
Q91250  
ID Q91250 PRELIMINARY; PRT; 632 AA.

Q91250; 01-MAR-2001 (TrEMBLrel. 16, Created)  
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
COPPER RESISTANCE PROTEIN A PRECURSOR.

PCOA OR PA2065.  
Pseudomonas aeruginosa.  
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
Pseudomonas.  
NCBI\_TaxID=287;  
GN

SEQUENCE FROM N.A.  
STRAIN=ATCC 15692 / PA01;  
MEDLINE=20437337; PubMed=10984043;  
Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y., Brody I.L., Coulter S.H., Wong K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.N., Fong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen."; *Nature* 406:959-964(2000).  
RA EMBL; AE004633; AAG05453.1; -.  
DR InterPro: IPR001117; Cu-oxidase.  
DR InterPro: IPR001287; Cu\_nit\_rdtctse.  
DR InterPro: IPR001993; Mitoch\_carrier.  
DR InterPro: IPR002355; MultiCu\_oxidse2.  
DR Pfam: PF00394; Cu-oxidase; 3.  
DR PRINTS; PR00695; CUNO2RDTASE.  
DR PROSITE; PS00215; MITOCH\_CARRIER; UNKNOWN\_1.  
DR PROSITE; PS00079; MULTICOPPER\_OXIDASE1; 1.  
DR PROSITE; PS00080; MULTICOPPER\_OXIDASE2; 1.  
DR Complete proteome.  
KW SEQUENCE 632 AA; 69851 MW; 229DA2AE86F5B519 CRC64;

Query Match 24.2%; Score 63; DB 16; Length 632;  
Best Local Similarity 34.3%; Pred. No. 5.7;  
Matches 12; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

**QY**            10 GSLPKSHGRQTQDENPVWHFFKNIVTPRTPTPPSQG 44  
       |::| ::|| :| ::||:  
**Dd**          451 GAMPMQHSPASEDCNPLVDMQMVTPTPKLADPGLG 485

[illegible]

CC07/10; Drosophila melanogaster (Fruit fly).  
OS Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.

RN	[1]	
RP		SEQUENCE FROM N.A.

STRAT=BERKELEY;  
MEDLINE=20196006; PubMed=10731132;  
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
Anatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
Sutton G.G., Wortman J.R., Randall M.D., Zhang Q., Chen L.X.,  
Brandon R.C., Rogers Y.-H.C., Blazer J.G., Champagne M., Pfeiffer B.D.,  
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
Cherry J.M., Cawley S., Dahlke B., Cadiou L.B., Davies P.,  
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I.I., Dietz S.M.,  
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,  
Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,  
Merkulov G., Milshina N.V., Mobbart C., Morris J., Moshrefi A.,  
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,  
RA Williams S.M., Woodgate T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:  
RT "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2185-2195(2000).  
RL EMBL; AE003537; AAF49800.1. -.  
SQ FLYBASE; FBgn0036377; CG10710.  
SQ SEQUENCE 709 AA; 78376 MW; 4A72C9FA67C671841 CRC64;

Query Match 23.8%; Score 62; DB 5; Length 709;  
Best Local Similarity 32.6%; Pred. NO. 8.8;  
Matches 14; Conservative 6; Mismatches 15; Indels 8; Gaps 1;

**Qy**            1   HHPARTAHYGLPQKSHGRTOENPVVHFKNIVTPRTPPSQ 43  
               || | | : : | | : : | | | |  
**Dd**          168   HHOALPAEVAHYAATGROOP-----RPVLPPRAPPSO 209

RESULT 5  
Q92576  
ID Q92576  
PRELIMINARY;  
PRT; 1723 AA.

AC	Q92576;	
AD	01-FEB-1997 (TREMBLrel. 02, Created)	
AE	01-FEB-1997 (TREMBLrel. 02, Last sequence update)	
AF	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
AG	KIAA0244 PROTEIN (FRAGMENT).	
AH	KIAA0244.	
AI	Homo sapiens (Human).	
AJ	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
AK	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AL	NCBI_TaxID=9606;	
AM	[1]	
AN	SEQUENCE FROM N.A.	
AO	TISSUE=BONE MARROW;	
AP	MEDLINE=37191544; PubMed=9039502;	
AQ	Nagase T., Seki N., Ishikawa K., Ohira M., Kawarabayasi Y., Ohara O.,	
AR	Tanaka A., Kotani H., Miyaajima N., Nomura N.:	
AS	"Prediction of the coding sequences of unidentified human genes. VI.	
AT	the coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by	
AV	analysis of cDNA clones from cell line KG-1 and brain.";	
AW	DNA Res. 3:321-329(1996).	
AX	EMBL; D87685; BAAL3438.1; -.	
AY	InterPro: IPR001965; PHD.	
AZ	InterPro: IPR003618; TFS2_cent.	
BA	Pfam: PF00628; PHD; 1.	
BB	SMART; SM00249; PHD; 1.	
BC	SMART; SM00510; TFS2M; 1.	
BD	NON_TER 1	
BE	SEQUENCE 1723 AA; 194625 MW; 042CEB335B89D9A4 CRC64;	
BF		
BG		
BH		
BI		
BJ		
BK		
BL		
BM		
BN		
BO		
BP		
BQ		
BR		
BS		
BT		
BU		
BV		
BW		
BX		
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BZ		
CA		
CB		
CC		
CD		
CE		
CF		
CG		
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CJ		
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CL		
CM		
CN		
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CB		
CC		
CD		
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CI		
CJ		
CK		
CL		
CM		
CN		
CO		
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CQ		
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CI		
CJ		
CK		
CL		
CM		
CN		
CO		
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CR		
CS		
CT		
CU		
CV		
CW		
CX		
CY		
CA		
CB		
CC		

Query Match 23.3%; Score 60.5; DB 4; Length 1723;  
Best Local Similarity 32.6%; Pred. No. 38;  
Matches 15; Conservative 4; Mismatches 12; Indels 15; Gaps 1;

QY 1 HHPARTAHYGLPQK-----SHGTQDENPVVHFFK 31  
 ||||:| || ||:|:|:| ||  
 Db 295 HHPAOTGHVSHSSOKCHKPOOAPAMKTNSHVKEELEHPGVEHFK 340

RESULT	6
Q9NQ16	
ID	Q9NQ16
AC	Q9NQ16;
	PRELIMINARY;
	PRT; 1957 AA.

DT	01-OCT-2000	(TREMBLrel. 15, Created)
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)
DE	DJ22117.1	(KIAA0244) (FRAGMENT).
DN	DJ22117.1	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_taxid=9606;	
RN	[1]	
RA	SEQUENCE FROM N.A.	
RA	Matthews L.;	
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.	
RL	EMBL: AL050329; CAB99358.1; -.	
DR	InterPro: IPR001965; PHD.	
DR	InterPro: IPR003618; TFS2_cent.	
DR	Tram: PF00628; PHD; 1.	
DR	SMART: SM00249; PHD; 1.	
DR	SMART: SM00510; TFS2M; 1.	
FT	NON_TER 1	
FO	SEQUENCE 1957 AA; 220419 MW; 90918EC75141632C CRC64;	

Query Match 23.3%; Score 60.5; DB 4; Length 1957;  
Best Local Similarity 32.6%; Pred. No. 44;  
Matches 15; Conservative 4; Mismatches 12; Indels 15; Gaps 1;

QY 1 HHPARTAHYGLSPQK-----SHGRTQDENPVVHFFK 31  
|||||:| | | | : : : | : | | |  
Db 529 HHPAQTGHVSHSSQKQCHKPOQQAAPAMKTNSHVKEELHPGVZHF 574

RESULT 7  
Q9UI45  
ID Q9UI45  
PRELIMINARY:  
PRT: 2039 AA.

AC	Q9UI45;
AD	01-MAY-2000 (TrEMBLrel. 13, Created)
AE	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
AF	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
AG	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
AH	PHD FINGER PROTEIN 3.
AI	PHF3.
AJ	HOMO
AK	Homo sapiens (Human).
AL	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AM	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AN	NCBI_TaxID=9606;
AO	[1]
AP	SEQUENCE FROM N.A.
AQ	Fischer U., Struss A.K., Hemmer D., Michel A., Meese E.;
AR	"Cloning of a novel gene localized on human chromosome 6q12 with
AS	decreased expression in malignant glioblastoma.";
AT	Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
AV	EMBL; AF091622; AAF21292.1; "
AW	DR InterPro; IPR001965; PHD.
AX	DR InterPro; IPR003618; TFS2_cent.
AY	DR Pfam; PF00628; PHD; 1.
AZ	DR SMART; SM00249; PHD; 1.
BA	DR SMART; SM00510; TFS2; 1.
BB	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
BC	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
BD	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
BE	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
BF	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
BG	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
BH	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
BI	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
BJ	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
BK	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
BL	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
BM	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
BN	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
BO	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
BP	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
BQ	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
BR	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
BS	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
BT	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
BU	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
BV	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
BW	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
BX	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
BY	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
BZ	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
CA	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
CB	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
CC	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
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CE	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
CF	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
CG	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
CH	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
CI	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
CJ	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
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CN	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
CO	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
CP	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
CQ	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
CR	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
CS	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
CT	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
CU	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
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CX	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
CY	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
CA	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
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CI	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
CJ	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
CK	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
CL	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
CM	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
CN	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9B CRC64;
CO	DR SMART; 2039 AA; 229480 MW; FDAFF00576005E9

Query Match 23.3%; Score 60.5; DB 4; Length 2039;  
Best Local Similarity 32.6%; Pred. No. 46;  
Matches 15; Conservative 4; Mismatches 12; Indels 15; Gaps 1;

QY 1 HHPARTAHYGLPQK-----SHGRTQDENPVVHFFK 31  
|||||:| | | | | : : : : | | |  
db 611 HHPAOTGHVSHSSOKOCHKPOOQAPAMKTNHSHVKEELHPGVVEHFK 656

RESULT	8	
Q95WV0		
ID	Q95WV0	PRELIMINARY;
AC	Q95WV0;	PRT; 676 AA.







DR EMBL; ALI62754; CAB84134.1; --  
 KW Complete proteome.  
 SQ SEQUENCE 556 AA; 60467 MW; A7A6D830BCE7C287 CRC64;

Query Match 22.7%; Score 59; DB 16; Length 556;  
 Best Local Similarity 35.9%; Pred. No. 17;  
 Matches 14; Conservative 2; Mismatches 23; Indels 0; Gaps 0;

OY 7 AHYGSLLPQKSHGRTQDENPVVHFFKNIVTPRTPPPSOGK 45  
 ||| | | | | | | | | | | | | | | | | | | |  
 Db 363 AAYAKYSPYHSRNRIRSNLEQRYKENIISTVPPSNGK 401

Search completed: August 28, 2002, 16:41:23  
 Job time: 375 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 28, 2002, 16:35:03 ; Search time 51.58 Seconds  
(without alignments)  
38.762 Million cell updates/sec

Title: US-09-813-383-1\_COPY\_8\_25  
Perfect score: 103  
Sequence: 1 HYGSLPQKSHGRQTQDENP 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_032802.\*  
1: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.\*  
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3: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.\*  
5: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.\*  
6: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.\*  
7: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.\*  
8: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.\*  
9: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.\*  
10: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.\*  
13: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.\*  
14: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.\*  
15: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.\*  
16: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.\*  
17: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.\*  
18: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	103	100.0	41	20 AAY04044	Human myelin basic
2	103	100.0	46	19 AAW72360	Human myelin basic
3	103	100.0	170	15 AAR48592	Human myelin basic
4	103	100.0	170	17 AAR95406	Myelin oligodendro
5	103	100.0	171	17 AAR97627	Human myelin basic
6	103	100.0	171	17 AAR99580	Human myelin basic
7	103	100.0	171	20 AAY27284	Human myelin basic
8	103	100.0	171	21 AAB19513	Human myelin basic
9	103	100.0	171	21 AAY69394	Amino acid sequenc
10	103	100.0	171	21 AAY44234	Human myelin basic
11	103	100.0	186	21 AAY57090	Human myelin basic

12	103	100.0	197	17 AAW00399	Human myelin basic
13	103	100.0	197	21 AAY95922	Human myelin bindi
14	103	100.0	203	17 AAW06107	Foetal myelin basi
15	103	100.0	203	17 AAW06108	Foetal myelin basi
16	103	100.0	373	17 AAW06103	MP4 chimeras (MBP21
17	103	100.0	375	17 AAW06104	MP4 chimeras (delta
18	103	100.0	385	17 AAW06102	MP3 chimeras (MBP21
19	103	100.0	492	17 AAW06105	MMOGP4 chimera (MB
20	97	94.2	168	15 AAR48594	Rabbit myelin basi
21	95	92.2	170	14 AAR35440	Human basic myelin
22	85	82.5	168	11 AAR04717	Empirically determ
23	85	82.5	170	14 AAR30736	Human MBP. Synthe
24	83.5	81.1	169	15 AAR48593	Cattle myelin basi
25	82	79.6	15	17 AAR91926	Peptide comprising
26	82	79.6	15	19 AAW72363	Human myelin basic
27	82	79.6	20	17 AAR95391	Residues 71-90 of
28	82	79.6	20	18 AAW4063	Human myelin basic
29	82	79.6	40	21 AAB12612	Human myelin basic
30	82	79.6	40	21 AAR5559	Human MBP peptide
31	78.5	76.2	127	15 AAR48596	Rat myelin basic p
32	78	75.7	39	21 AAY85561	Human MBP peptide
33	75.5	73.3	170	11 AAR02226	Myelin basic prote
34	75.5	73.3	170	14 AAR30735	Bovine MBP. Syn
35	75.5	73.3	170	15 AAR45947	Myelin basic prote
36	75.5	73.3	170	17 AAR86422	Myelin basic prote
37	75.5	73.3	170	19 AAW57236	Myelin basic prote
38	75.5	73.3	170	21 AAY58368	Mammalian generic
39	74	71.8	20	17 AAR55350	Residues 61-80 of
40	74	71.8	20	18 AAW44062	Human myelin basic
41	74	71.8	20	20 AAW73615	Human myelin basic
42	74	71.8	20	21 AAB12624	Human myelin basic
43	74	71.8	20	21 AAY85556	Human MBP peptide
44	67	65.0	20	19 AAW78824	Myelin basic prote
45	67	65.0	20	21 AAB33636	MHC class II assoc

## ALIGNMENTS

RESULT 1  
AAY04044  
ID AAY04044 standard; peptide; 41 AA.

XX AC AAY04044;

XX DT 20-DEC-1999 (first entry)

XX DE Human myelin basic protein residues 60-100.

XX KW Multiple sclerosis; MS; demyelinating disease; treatment; diagnosis;  
antigen; myelin basic protein; MBP; antibody; epitope.

XX OS Homo sapiens.

XX PN CA2201274-A.

XX PD 27-SEP-1998.

XX PF 27-MAR-1997; 97CA-2201274.

XX PR 27-MAR-1997; 97CA-2201274.

XX PA (UYBR-) UNIV BRITISH COLUMBIA.

XX PI McGeer PL, Lee G, McGeer EG;

XX DR WPI; 1999-591471/51.

XX PT Treating multiple sclerosis by administering specific peptides.

XX PS Disclosure; Page 15; 18pp; English.

XX CC A new method is disclosed for treating multiple sclerosis and other

CC demyelinating diseases in humans. The method comprises administering  
 CC a combination of peptides of less than 15 amino acids, designed to  
 CC neutralize the antigenic effects of exposed epitopes in degenerating  
 CC myelin. The epitopes are identified using immunohistochemical analysis  
 CC of affected tissue with prepared antibodies. The peptides are mimics  
 CC which block autoantibodies, and complementary or binding peptides to  
 CC block the exposed antigenic epitopes. Preferably the exposed epitope  
 CC on degenerating myelin is QDENPVV and the peptide to be administered  
 CC is (a) QDENPVV, (b) dQ-DENPVV-dV, (c) R1-QDENPVV-R2, (d) DYGVFIL, (e)  
 CC dQ-YGVFI-dL or (f) R1-DYGVFIL-R2; where R1 and R2 are peptides of 1-4  
 CC amino acid residues. The peptide QDENPVV corresponds to human myelin  
 CC basic protein residues 82-88, and the peptide DYGVFIL is a complementary  
 CC peptide to QDENPVV, i.e. it is encoded by the cDNA strand complementary  
 CC to that which codes for QDENPVV. The invention also extends to a  
 CC method for diagnostic differentiation between normal and degenerating  
 CC myelin, using antibodies that recognize the sequence QDENPVV.

XX Sequence 41 AA;

Query Match 100.0%; Score 103; DB 20; Length 41;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYGSLPQKSHGRQTQDENP 18  
 |||||  
 Db 10 hygslpqkshgrtqdenp 27

RESULT 2

AAW72360  
 ID AAW72360 standard; peptide; 46 AA.

AC AAW72360;

XX 16-DEC-1998 (first entry)

XX Human myelin basic protein fragment.

XX Human; myelin basic protein; MBP; multiple sclerosis; anti-MBP; MS.

XX Homo sapiens.

XX WO9845327-A1.

XX 15-OCT-1998.

XX 03-APR-1998; 98WO-CA00290.

XX 04-APR-1997; 97CA-2201841.

XX (UYAL-) UNIV ALBERTA.

XX Catz I, Warren KG;

XX WPI; 1998-568336/48.

XX Peptide and its derivatives for treatment of multiple sclerosis - is  
 PT capable of neutralising or modulating production of anti-myelin  
 PT basic protein

XX Disclosure; Page 15; 75pp; English.

XX The present sequence represents a myelin basic protein (MBP) protein  
 CC fragment used to produce MBP peptides. MBP peptides are capable of  
 CC neutralising or modulating the production of anti-myelin basic protein.  
 CC The present invention also describes a method for treating multiple  
 CC sclerosis (MS). The method comprises administering to the patient an  
 CC MBP peptide of the formula: R1-Vai-His-Phe-Phe-Lys-Asn-Ile-R2 where R1,  
 CC R2 = H, OH, or an amino acid residue and a polypeptide residue,  
 CC provided that R1 and R2 are not both H or OH at the same time.

XX Sequence 46 AA;

Query Match 100.0%; Score 103; DB 19; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYGSLPQKSHGRQTQDENP 18  
 |||||  
 Db 8 hygslpqkshgrtqdenp 25

RESULT 3

AAAR48592  
 ID AAR48592 standard; protein; 170 AA.

XX AAR48592;

XX 31-JUL-1994 (first entry)

XX Human myelin basic protein.

XX Proteolipid protein; myelin basic protein; retrovirus;

XX neurological disease; by-stander antigen; TGF-beta;

XX transforming growth factor-beta; T-cell; T-lymphocyte;

XX myelopathy; paraparesis; human immunodeficiency virus type 1.

XX Homo sapiens.

XX WO9404121-A.

XX 03-MAR-1994.

XX 17-AUG-1993; 93WO-US07786.

XX 17-AUG-1992; 92US-0931217.

XX (AUTO-) AUTOIMMUNE INC.

XX Hafler DA, Weiner HL;

XX WPI; 1994-082786/10.

XX Treating retroviral associated neurological disease - by admin.  
 PT of by-stander antigen, causing release of transforming growth  
 PT factor beta from suppressor T cells

XX Disclosure; Page 49; 64pp; English.

XX Myelin basic proteins (sequences AAR48592-96) and cattle proteolipid  
 CC protein (AAR48592) elicit the release of TGF-beta from suppressor T-  
 CC cells and target the T-cells to neural tissue under cytotoxic  
 CC attack, thereby reducing neurological disease, e.g. HTLV-1  
 CC associated myelopathy, tropical spastic paraparesis and HIV  
 CC infection.

XX Sequence 170 AA;

Query Match 100.0%; Score 103; DB 15; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYGSLPQKSHGRQTQDENP 18  
 |||||  
 Db 68 hygslpqkshgrtqdenp 85

RESULT 4

AAAR95406  
 ID AAR95406 standard; protein; 170 AA.

XX AAR95406;

XX

DT 16-DEC-1996 (first entry)  
 XX Myelin oligodendrocyte protein.  
 XX  
 XX Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE;  
 KW CD4+; T-cell; autoimmune disease; demyelination; central nervous system;  
 KW CNS; animal model; human; multiple sclerosis; MS; mammal; benign MS; MOG;  
 KW relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PLP;  
 KW diabetes; Graves disease; myasthenia gravis; Good Pasture's syndrome;  
 KW psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG;  
 KW myelin oligodendrocyte protein; myelin associated glycoprotein; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO9612737-A2.  
 PN  
 XX  
 XX 02-MAY-1996.  
 PD  
 XX  
 XX 25-OCT-1995; 95WO-US13682.  
 PF  
 XX  
 XX 15-MAR-1995; 95US-0404228.  
 PR  
 XX 25-OCT-1994; 94US-0328224.  
 PR  
 XX 25-OCT-1995; 95ZA-0009033.  
 PR  
 XX (IMMU-) IMMULOGIC PHARM CORP.  
 PA  
 XX Devaux B, Franzen H, Geffer M, Hsu D, Pallard X;  
 PI Rothbard J, Samson M, Shi J, Smilek D;  
 PI  
 XX WPI: 1996-230552/23.  
 DR  
 XX  
 XX Myelin basic derived peptide(s) and analogs - used in the treatment  
 PT of Multiple Sclerosis, psoriasis, Graves Disease, etc.  
 PT  
 XX  
 PS Example 9; Fig 1; 91pp; English.  
 XX  
 XX This sequence represents the human myelin oligodendrocyte protein (MOG).  
 CC Immunisation with MOG (or the peptide fragments shown in  
 CC AAR95375-R95385) can be used to induce experimental allergic  
 CC encephalomyelitis (EAE) in susceptible strains of mice. EAE is a CD4+  
 CC T-cell mediated autoimmune disease which results in demyelination of the  
 CC central nervous system, resulting in paralysis and other neurological  
 CC abnormalities. EAE is a commonly used animal model for human multiple  
 CC sclerosis (MS). These sequences can be used in compositions for treating  
 CC MS in a mammal. The composition acts to down regulate the autoimmune  
 CC response, and may be administered in an amount sufficient to prevent the  
 CC onset of symptoms of MS. The compositions may also be used to treat  
 CC advanced stage MS, especially relapsing-remitting MS, chronic progressive  
 CC MS or benign MS. These peptides may also be used in the treatment of  
 CC other diseases involving myelin autoantigens, including diabetes, Graves  
 CC disease, myasthenia gravis, Good Pasture's syndrome, psoriasis,  
 CC thyroiditis, and rheumatoid arthritis. Peptides derived from other  
 CC myelin autoantigens, such as myelin basic protein (MBP, see  
 CC AAR95334-R95374), proteolipid protein (PLP), and myelin associated  
 CC glycoprotein (MAG) can be used as alternatives to the MOG peptides in  
 CC these compositions.  
 XX  
 XX Sequence 170 AA;  
 SQ  
 Query Match 100.0%; Score 103; DB 17; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HYGSLPQKSHGRTOENP 18  
 Db | | | | | | | | | | | | | | | | | |  
 68 hyslplqkshgrtqdenp 85  
 RESULT 5  
 AAR97627  
 ID AAR97627 standard; Protein; 171 AA.  
 XX

AC AAR97627;  
 XX  
 XX 09-NOV-1996 (first entry)  
 XX  
 XX Human myelin basic protein.  
 XX  
 XX Myelin basic protein; MBP; multiple sclerosis; MS; treatment;  
 KW prevention; analogue.  
 KW  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT Peptide 86..99  
 FT /label= Claimed peptide region.  
 XX  
 XX WO9616085-A1.  
 PN  
 XX  
 XX 30-MAY-1996.  
 PD  
 XX  
 XX 16-NOV-1995; 95WO-US14402.  
 PF  
 XX  
 XX 18-NOV-1994; 94US-0342078.  
 PR  
 XX (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 PA (STRD) UNIV STANFORD MEDICAL CENT.  
 PA  
 XX Conlon PJ, Gaur A, Ling N, Steinman L;  
 PI  
 XX WPI: 1996-268534/27.  
 DR N-PSDB; AAT30269.  
 DR  
 XX  
 XX Peptide analogue of human myelin basic protein - has Lysine 91  
 PT replaced by another amino acid, useful to treat multiple sclerosis  
 PT  
 XX  
 XX Claim 1; Figure 1; 30pp; English.  
 PS  
 XX  
 XX A peptide analogue comprising amino acids 87-99 of human myelin  
 CC basic protein (MBP), where lys91 is substituted for another amino  
 CC acid can be used to treat and prevent multiple sclerosis. The  
 CC peptide analogue is administered at a dosage range of 5-50 mg/kg.  
 XX  
 XX Sequence 171 AA;  
 SQ  
 Query Match 100.0%; Score 103; DB 17; Length 171;  
 Best Local Similarity 100.0%; Pred. No. 7.7e-10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HYGSLPQKSHGRTOENP 18  
 Db | | | | | | | | | | | | | | | | | |  
 69 hyslplqkshgrtqdenp 86  
 RESULT 6  
 AAR99580  
 ID AAR99580 standard; Protein; 171 AA.  
 XX  
 XX AAR99580;  
 AC  
 XX  
 XX 07-NOV-1996 (first entry)  
 DT  
 XX  
 XX Human myelin basic protein (MBP).  
 DE  
 XX  
 XX Myelin basic protein; MBP; multiple sclerosis; MS; competition;  
 KW inhibition; major histocompatibility complex; MHC; thymocyte; T cell;  
 KW experimental allergic encephalomyelitis; EAE; analogue.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO9616086-A1.  
 PN  
 XX  
 XX 30-MAY-1996.  
 PD  
 XX

PP 16-NOV-1995; 95WO-US14403.  
 XX 18-NOV-1994; 94US-0342408.  
 PR (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 XX  
 PA Conlon PJ, Gaur A, Ling N, Steinman L;  
 XX WPI; 1996-268535/27.  
 XX N-PSDB; AAT32561.  
 DR  
 XX  
 PT Peptide analogues of human myelin basic protein - useful for  
 PT treatment of multiple sclerosis  
 XX  
 PS Disclosure; Figure 1; 61pp; English.  
 XX  
 CC Peptide analogues comprising at least seven amino acids from  
 CC residues 86-99 of human myelin basic protein (MBP), can be used to  
 CC treat multiple sclerosis by competing for the binding of native MBP  
 CC peptide to MHC and by not causing proliferation of an MBP reactive T-  
 CC cell line. The peptide analogues also inhibit the induction of  
 CC experimental allergic encephalomyelitis (EAE) by MBP in rodents.  
 CC The peptide analogues have a reduced susceptibility to proteolysis  
 CC in vivo.  
 XX  
 SQ Sequence 171 AA;  
 Query Match 100.0%; Score 103; DB 17; Length 171;  
 Best Local Similarity 100.0%; Pred. No. 7.7e-10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HYGSLPQKSHGRTQDENP 18  
 DB 69 hygslpqkshgtrtqdenp 86  
 RESULT 7  
 AAY27284  
 ID AAY27284 standard; Protein; 171 AA.  
 XX  
 AC AAY27284;  
 XX  
 DT 29-OCT-1999 (first entry)  
 XX  
 DE Human myelin basic protein (MBP).  
 XX  
 KW Myelin basic protein; MBP; peptide analogue; MHC; multiple sclerosis;  
 KW T-cell reactivity; major histocompatibility complex; human.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 86..99  
 FT /note= "peptide analogues of the invention comprise  
 FT at least seven consecutive amino acid residues  
 FT from this region"  
 FT  
 FT Misc-difference 97  
 FT /note= "the L-Arg at this position can be altered to  
 FT a D-amino acid and especially to a D-Ala to  
 FT construct the peptide analogues (see claims 2  
 FT and 3"  
 FT  
 PN US5948764-A.  
 XX  
 XX 07-SEP-1999.  
 XX  
 XX 09-JAN-1997; 97US-0781122.  
 XX  
 XX 09-JAN-1997; 97US-0781122.  
 XX 09-MAR-1995; 95US-0402992.  
 XX  
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.

XX Conlon PJ, Gaur A, Ling N;  
 XX WPI; 1999-517966/43.  
 DR N-PSDB; AA200399.  
 XX  
 XX Human myelin basic protein analogues useful for the treatment of  
 XX multiple sclerosis  
 XX  
 PS Disclosure; Fig 1; 35pp; English.  
 XX  
 CC The invention provides human myelin basic protein (MBP) analogues. The  
 CC analogues, comprise a sequence of 7 or more consecutive amino acids  
 CC taken from between residues 86 to 99 of the native human MBP amino acid  
 CC sequence (AAY27284). The analogues include residue 97 of the human MBP  
 CC sequence, however, the L-arginine at position 97 is altered to a D-amino  
 CC acid. The peptide analogues may be used for treating multiple sclerosis.  
 CC Multiple sclerosis may be caused by an autoimmune reaction involving  
 CC T-cells which have lost their 'self-tolerance' and attack normal tissue.  
 CC Therefore, T-cell reactivity to human MBP may be a major cause of the  
 CC development of MS. The T-cells recognize and bind to an epitope of the  
 CC MBP between amino acids 86 to 106 of the sequence. The peptide analogues  
 CC have a higher binding affinity for major histocompatibility complexes  
 CC (MHC) on the T-cells than human MBP and therefore interfere with the  
 CC reactivity of T-cells against human MBP. Administration of the analogues  
 CC may prevent future, repeated attacks of multiple sclerosis without any  
 CC side effects after long-term use (such as malignancies, toxic hepatitis  
 CC and immunocompromising the patient). The present sequence represents a  
 CC human MBP sequence.  
 XX  
 SQ Sequence 171 AA;  
 Query Match 100.0%; Score 103; DB 20; Length 171;  
 Best Local Similarity 100.0%; Pred. No. 7.7e-10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HYGSLPQKSHGRTQDENP 18  
 DB 69 hygslpqkshgtrtqdenp 86  
 RESULT 8  
 AAB19513  
 ID AAB19513 standard; Protein; 171 AA.  
 XX  
 AC AAB19513;  
 XX  
 DT 09-JAN-2001 (first entry)  
 XX  
 DE Human myelin basic protein.  
 XX  
 KW Myelin basic protein; human; autoimmune disease; autoantigen;  
 KW demyelinating disease; experimental autoimmune encephalitis;  
 KW multiple sclerosis; antiinflammatory; DNA vaccination; vaccine;  
 KW T cell; pro-inflammatory response.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200053019-A1.  
 XX  
 PD 14-SEP-2000.  
 XX  
 PF 10-MAR-2000; 2000WO-US06233.  
 XX  
 PR 12-MAR-1999; 99US-0267590.  
 XX  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 XX  
 PI Steinman L, Ruiz PJ, Garren H;  
 XX  
 XX WPI; 2000-587361/55.  
 DR N-PSDB; AAA50667.

XX Treating an autoimmune disease in a mammalian host by introducing a DNA  
 PT expression cassette comprising a sequence encoding a portion of an  
 PT autoantigen associated with a pro-inflammatory Th1-type T cell response  
 PT  
 XX  
 XX Disclosure: Page 42; 50pp; English.  
 XX  
 CC The present sequence is that of human myelin basic protein. The  
 CC invention provides methods for the suppression of pro-inflammatory  
 CC T cell responses in autoimmune disease. A mammalian host is  
 CC vaccinated with a DNA expression vector encoding an autoantigen  
 CC fragment, e.g. from myelin basic protein. In response to the  
 CC vaccination, pathogenic T cell proliferation is inhibited and  
 CC production of Th1 cytokines, including interleukin-2,  
 CC interferon-gamma and interleukin-15, is reduced. Suppressive  
 CC vaccination diminishes T cell pro-inflammatory responses in a  
 CC specific, targeted manner. Conditions that benefit from this  
 CC treatment include autoimmune diseases, tissue transplantation and  
 CC other conditions associated with inflammation. Autoimmune  
 CC diseases that can be treated include demyelinating diseases such as  
 CC experimental autoimmune encephalitis and multiple sclerosis  
 CC (claimed).  
 XX

SQ Sequence 171 AA;

Query Match 100.0%; Score 103; DB 21; Length 171;  
 Best Local Similarity 100.0%; Pred. No. 7.7e-10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HYGSLPQKSHGRTQDENP 18  
 | | | | | | | | | | | | | | | | | |  
 Db 69 hygslpqkshgtrtdenp 86

RESULT 9

AAAY69394  
 ID AAY69394 standard; Protein; 171 AA.  
 XX  
 AC AAY69394;  
 XX  
 DT 19-JUN-2000 (first entry)  
 XX  
 DE Amino acid sequence of a human myelin basic protein.  
 XX  
 KW Human; myelin basic protein; oligodendroglial cell; Th2 immune response;  
 KW Th2-type cytokine; analogue; multiple sclerosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200011027-A1.  
 XX  
 PD 02-MAR-2000.  
 XX  
 PF 19-AUG-1999; 99WO-US19033.  
 XX  
 PR 20-AUG-1998; 98US-0137759.  
 XX  
 PA (NOVS ) NOVARTIS AG.  
 PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 XX  
 PI Gaur A, Conlon P, Ling NC, Staehlin T, Crowe P;  
 XX  
 XX WPI; 2000-224661/19.  
 DR N-PSDB; AA261594.  
 XX  
 XX Inducing a Th2 immune response and a persistent systemic immune  
 PT response to myelin basic protein, MBP, or a peptide analog of MBP for  
 PT use in treating multiple sclerosis, by administering compositions  
 PT comprising peptide analogs of MBP  
 PT  
 XX

PS Disclosure; Fig 1; 112pp; English.

XX The present sequence represents a human myelin basic protein. Myelin  
 CC basic protein is found in the cytoplasm of human oligodendroglial  
 CC cells. Peptide analogues of myelin basic protein are administered to  
 CC a patient in need to induce a Th2 immune response (i.e. production  
 CC of T cells producing one or more Th2-type cytokines) and/or a  
 CC persistent systemic immune response to myelin basic protein. These  
 CC peptide analogues are at least seven amino acids long, derived from  
 CC residues 83-99 of human myelin basic protein and altered from the  
 CC native sequence at least at positions 91, 95 or 97. The peptide  
 CC analogs are especially useful in the treatment of multiple sclerosis.  
 XX

SQ Sequence 171 AA;

Query Match 100.0%; Score 103; DB 21; Length 171;  
 Best Local Similarity 100.0%; Pred. No. 7.7e-10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HYGSLPQKSHGRTQDENP 18  
 | | | | | | | | | | | | | | | | | |  
 Db 69 hygslpqkshgtrtdenp 86

RESULT 10

AAAY44234  
 ID AAY44234 standard; Protein; 171 AA.  
 XX  
 AC AAY44234;  
 XX  
 DT 21-FEB-2000 (first entry)  
 XX  
 DE Human myelin basic protein.  
 XX  
 KW Human; myelin basic protein; MBP; NS-specific antigen;  
 KW nervous system-specific antigen; T cell; peripheral nervous system; PNS;  
 KW central nervous system; CNS; nerve regeneration; neuronal degeneration;  
 KW spinal cord injury; blunt trauma; penetrating trauma; senile dementia;  
 KW ischaemic stroke; diabetic neuropathy; glaucoma; haemorrhagic stroke;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's chorea;  
 KW amyotrophic lateral sclerosis; ALS; treatment.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT Peptide  
 FT /label= Cryptic epitope  
 FT /note= "activates T cells by itself but does not  
 FT induce an autoimmune disease"  
 FT Peptide  
 FT 51..70  
 FT /label= Cryptic epitope  
 FT /note= "activates T cells by itself but does not  
 FT induce an autoimmune disease"  
 FT Peptide  
 FT 91..110  
 FT /label= Cryptic epitope  
 FT /note= "activates T cells by itself but does not  
 FT induce an autoimmune disease"  
 FT Peptide  
 FT 131..150  
 FT /label= Cryptic epitope  
 FT /note= "activates T cells by itself but does not  
 FT induce an autoimmune disease"  
 FT Peptide  
 FT 151..170  
 FT /label= Cryptic epitope  
 FT /note= "activates T cells by itself but does not  
 FT induce an autoimmune disease"  
 XX  
 PN WO9960021-A2.  
 XX  
 XX 25-NOV-1999.  
 XX  
 XX 19-MAY-1999; 99WO-US10953.  
 XX

(ALEX-) ALEXION PHARM INC.  
(USSH) US DEPT HEALTH & HUMAN SERVICES.



XX Lenardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;  
 PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;  
 XX WPI: 1996-505898/50.  
 DR N-PSDB; AAT41889.  
 XX New human myelin basic protein and proteolipid protein variant(s) -  
 PT used in the assessment, diagnosis and treatment of multiple  
 PT sclerosis  
 XX  
 PS Claim 1; Page 79-80; 156pp; English.  
 XX  
 CC The native human 21.5 kDa foetal isoform (AAW00399) of myelin basic  
 CC protein, MBP+X2Cys81, includes an exon 2-encoded region (X2) that  
 CC may contain an epitope involved in the pathogenesis of multiple  
 CC sclerosis (MS); the X2 region is not found in the MBP of healthy  
 CC adults. Recombinant MBP+X2, or variants modified to improve  
 CC bacterial expression (see also AAW06107), can be produced in a  
 CC large scale in bacterial hosts. They are useful for assaying  
 CC T-cells for responsiveness to MBP epitopes and can be used as  
 CC therapeutic agents that act by inducing T-cell responses,  
 CC including energy and apoptosis, as a means of treating MS.  
 XX  
 XX Sequence 197 AA;  
 SQ

Query Match 100.0%; Score 103; DB 17; Length 197;  
 Best Local Similarity 100.0%; Pred. No. 9e-10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTDQNP 18  
 Db | | | | | | | | | | | | | | | | | |  
 95 hygslpqkshgrtqdenp 112

RESULT 13  
 AAY95922  
 ID AAY95922 standard; Protein; 197 AA.  
 XX  
 AC AAY95922;  
 XX  
 XX 20-NOV-2000 (first entry)  
 DT  
 XX Human myelin binding protein Delta II.  
 DE  
 XX Myelin binding protein; MBP; human; GPBP;  
 KW goodpasture antigen binding protein; autoimmune disease; apoptosis;  
 KW cancer; tumour; therapy.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO2000050607-A2.  
 PN  
 XX 31-AUG-2000.  
 PD  
 XX 24-FEB-2000; 2000WO-IB00324.  
 PF  
 XX 24-FEB-1999; 99US-0121483.  
 PR  
 XX (SAUS/) SAUS J.  
 PA  
 XX Saus J;  
 XX  
 XX WPI: 2000-572094/53.  
 DR N-PSDB; AAW50371.  
 XX  
 XX Novel Goodpasture antigen binding proteins useful for diagnosing and  
 PT treating autoimmune disorders, tumor, and preventing cell apoptosis -  
 PT  
 XX  
 PS Claim 36; Page 157; 158pp; English.  
 XX  
 CC The present sequence is that of human myelin binding protein (MBP)

CC Delta II, i.e. an alternative form of human MBP resulting from  
 CC splicing out of exon II. The protein was recombinantly expressed in  
 CC Pichia pastoris cells. The invention relates to novel Goodpasture  
 CC antigen binding proteins (GPBPs, see AAY95900-11), which bind to and  
 CC phosphorylate the unique N-terminal region of human GP, and which  
 CC are highly expressed in several autoimmune conditions. Claimed  
 CC methods for treating an autoimmune disorder, cell apoptosis or a  
 CC tumour involve modifying the expression or activity of GPBP,  
 CC especially using a MBP protein or a nucleic acid sequence encoding  
 CC it.  
 XX  
 XX Sequence 197 AA;  
 SQ

Query Match 100.0%; Score 103; DB 21; Length 197;  
 Best Local Similarity 100.0%; Pred. No. 9e-10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTDQNP 18  
 Db | | | | | | | | | | | | | | | | | |  
 95 hygslpqkshgrtqdenp 112

RESULT 14  
 RAW06107  
 ID AAW06107 standard; Protein; 203 AA.  
 XX  
 AC AAW06107;  
 XX  
 DT 01-FEB-1997 (first entry)  
 XX  
 DE Foetal myelin basic protein MBP+X2Cys81/bact.  
 XX  
 XX Myelin basic protein; MBP; MBP+X2Cys81; proteolipid protein; PLP;  
 KW multiple sclerosis; autoimmune disease; diagnosis; therapy;  
 KW T-lymphocyte; T-cell; anergy; apoptosis.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT 60..85  
 FT Region /label= X2  
 FT /note= "exon 2-encoded region"  
 FT  
 XX WO9634622-A1.  
 PN  
 XX 07-NOV-1996.  
 PD  
 XX 22-APR-1996; 96WO-US05611.  
 PF  
 XX 07-JUN-1995; 95US-0482114.  
 PR 02-MAY-1995; 95US-0431644.  
 PR 02-MAY-1995; 95US-0431648.  
 XX  
 PA (ALEX-) ALEXION PHARM INC.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 XX Lenardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;  
 PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;  
 XX  
 XX WPI: 1996-505898/50.  
 DR N-PSDB; AAT41896.  
 XX  
 XX New human myelin basic protein and proteolipid protein variant(s) -  
 PT used in the assessment, diagnosis and treatment of multiple  
 PT sclerosis  
 PT  
 XX  
 PS Disclosure; Page 81-82; 156pp; English.  
 XX  
 CC A 21.5 kDa foetal isoform (AAW06107) of myelin basic protein,  
 CC MBP+X2Cys81/bact., is the product of a DNA construct (AAT41896)  
 CC based on the human foetal MBP+X2Cys81 isoform (AAW00399) but  
 CC utilising bacterially-preferred codons in place of the native human

CC codons (see also AAT41889). This increases prodn. of the MBP in E.  
 CC coli by at least 50%. Recombinant MBP 21.5 polypeptides (see also  
 CC AAW00399 and AAW06108) are useful in the clinical assessment, diagnosis  
 CC and treatment of MS.

XX Sequence 203 AA;

Query Match 100.0%; Score 103; DB 17; Length 203;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18  
 |||||  
 Db 95 hygslpqkshgrtgdenp 112

# RESULT 15

AAW06108  
 ID AAW06108 standard; Protein; 203 AA.

XX AC AAW06108;

XX DT 01-FEB-1997 (first entry)

XX DE Foetal myelin basic protein MBP+X2Ser81/bact.

XX KW Myelin basic protein; MBP; MBP+X2Ser81; proteolipid protein; PLP;  
 KW multiple sclerosis; autoimmune disease; diagnosis; therapy;  
 KW T-lymphocyte; T-cell; anergy; apoptosis.

XX OS Synthetic.

XX FH Key Location/Qualifiers  
 FT Region 60..85

FT /label= X2  
 FT /note= "exon 2-encoded region, with Cys81Ser  
 FT mutation"

FT Peptide

FT 198..203  
 FT /label= Hexa-histidine-tag  
 FT /note= "the hexa-histidine tag facilitates  
 FT purification of the recombinant protein  
 FT from host cells"

XX PN WO9634622-A1.

XX PD 07-NOV-1996.

XX PF 22-APR-1996; 96WO-US05611.

XX PR 07-JUN-1995; 95US-0482114.

XX PR 02-MAY-1995; 95US-0431644.

XX PR 02-MAY-1995; 95US-0431648.

XX PA (ALEX-) ALEXION PHARM INC.

XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX PI Leonardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;  
 PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;

XX DR WPI; 1996-505898/50.

XX DR N-PSDB; AAT41897.

XX PT New human myelin basic protein and proteolipid protein variant(s) -  
 PT used in the assessment, diagnosis and treatment of multiple  
 PT sclerosis

XX PS Disclosure; Page 82-83; 156pp; English.

XX CC A 21.5 kDa foetal isoform (AAW06108) of myelin basic protein.  
 CC MBP+X2Ser81/bact., is the product of a DNA construct (AAT41897)  
 CC based on the human foetal MBP+X2Cys81 isoform (AAW00399) but  
 CC utilising codons that are highly expressed in bacterial genes in

CC place of the native codons (see also AAT41889) and incorporating a  
 CC sequence coding for a hexa-histidine tail. This allows large-  
 CC scale prodn. and purification of the MBP in bacterial hosts.  
 CC Recombinant MBP 21.5 polypeptides (see also AAW00399 and AAW06107) are  
 CC useful in the clinical assessment, diagnosis and treatment of MS.

XX Sequence 203 AA;

Query Match 100.0%; Score 103; DB 17; Length 203;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18  
 |||||  
 Db 95 hygslpqkshgrtgdenp 112

Search completed: August 28, 2002, 16:35:03  
 Job time: 285 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 28, 2002, 16:35:30 ; Search time 20.54 Seconds  
(without alignments)  
21.405 Million cell updates/sec

Title: US-09-813-383-1\_COPY\_8\_25

Perfect score: 103

Sequence: 1 HYGSLPQKSHGRTQDENP 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pap:\*

2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pap:\*

3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pap:\*

4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pap:\*

5: /cgn2\_6/ptodata/2/1aa/PTCUS.COMB.pap:\*

6: /cgn2\_6/ptodata/2/1aa/backfiles1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	103	100.0	170	2	US-08-327-357A-1
2	103	100.0	170	3	US-09-007-520-1
3	103	100.0	170	4	US-09-055-263-1
4	103	100.0	170	4	US-09-007-520-1
5	103	100.0	170	4	US-08-342-408B-2
6	103	100.0	171	2	US-08-781-122-2
7	103	100.0	171	4	US-09-137-759-2
8	85	82.5	168	6	5194425-4
9	82	79.6	20	3	US-08-297-395-21
10	82	79.6	40	3	US-08-297-395-2
11	75.5	73.3	170	1	US-08-227-372-1
12	75.5	73.3	170	3	US-08-462-351-3
13	75.5	73.3	170	6	5194425-3
14	75.5	73.3	170	6	5468481-3
15	74.5	72.3	170	3	US-08-470-397-1
16	74	71.8	20	2	US-08-468-540B-8
17	74	71.8	20	3	US-08-297-395-20
18	67	65.0	20	1	US-08-787-547-35
19	66.5	64.6	17	4	US-09-123-485-1
20	66	64.1	20	2	US-08-468-540B-7
21	63.5	61.7	19	4	US-09-153-586-30
22	59.5	57.8	19	4	US-09-153-586-25
23	58.5	56.8	13	2	US-08-596-387B-9
24	58.5	56.8	13	4	US-09-067-615-9
25	58.5	56.8	13	5	PCT-US95-09816A-9
26	54.5	52.9	15	2	US-08-735-253-18
27	53.5	51.9	18	2	US-08-468-540B-14

28	49.5	48.1	37	4	US-09-153-586-4	Sequence 4, Appli
29	48	46.6	9	3	US-08-159-339A-1079	Sequence 1079, Ap
30	46	44.7	10	3	US-08-159-339A-1096	Sequence 1096, Ap
31	45	43.7	23	1	US-08-787-547-1	Sequence 1, Appli
32	45	43.7	24	1	US-08-305-871A-2	Sequence 2, Appli
33	45	43.7	24	2	US-08-480-190-46	Sequence 46, Appl
34	45	43.7	24	2	US-08-488-379-46	Sequence 46, Appl
35	45	43.7	24	5	PCT-US93-07545-46	Sequence 46, Appl
36	44	42.7	1312	4	US-09-041-886-19	Sequence 19, Appl
37	42	40.8	1865	1	US-08-588-985-2	Sequence 2, Appli
38	42	40.8	1865	1	US-08-571-988-2	Sequence 2, Appli
39	41.5	40.3	475	2	US-08-819-825-2	Sequence 2, Appli
40	41.5	40.3	475	4	US-09-163-642-2	Sequence 19, Appl
41	41	39.8	107	4	US-08-327E-19	Sequence 19, Appl
42	41	39.8	107	4	US-08-462-625-19	Sequence 19, Appl
43	41	39.8	117	4	US-08-098-327E-20	Sequence 20, Appl
44	41	39.8	117	4	US-08-462-625-20	Sequence 20, Appl
45	41	39.8	316	4	US-08-098-327E-31	Sequence 31, Appl

## ALIGNMENTS

RESULT 1  
US-08-327-357A-1  
; Sequence 1, Application US/08327357A  
; Patent No. 5817629  
; GENERAL INFORMATION:

APPLICANT: WARREN, Kenneth G.  
APPLICANT: CATZ, Ingrid

TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC

TITLE OF INVENTION: PROTEIN AND THE ADMINISTRATION OF MYELIN BASIC PROTEIN

TITLE OF INVENTION: PEPTIDES TO MULTIPLE SCLEROSIS PATIENTS

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti

STREET: 1201 New York Avenue, N.W., Suite 1000

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/327,357A

FILING DATE: 21-OCT-1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/798,099

FILING DATE: 27-NOV-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: CA 2,053,799-0

FILING DATE: 22-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 27052-115469

TELEPHONE: 202-962-4810

TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 170 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

IMMEDIATE SOURCE:

CLONE: human myelin basic protein  
US-08-327-357A-1

Query Match 100.0%; Score 103; DB 2; Length 170;  
Best Local Similarity 100.0%; Pred. No. 3.6e-10;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18  
|||||

Db 68 HYGSLPQKSHGRTQDENP 85

## RESULT 2

US-09-007-520-1  
; Sequence 1, Application US/09007520  
; Patent No. 6103696  
; GENERAL INFORMATION:  
; APPLICANT: WARREN, Kenneth G.  
; APPLICANT: CATZ, Ingrid  
; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC  
; TITLE OF INVENTION: PROTEIN AND THE ADMINISTRATION OF MYELIN BASIC PROTEIN  
; TITLE OF INVENTION: PEPTIDES TO MULTIPLE SCLEROSIS PATIENTS  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
; STREET: 1201 New York Avenue, N.W., Suite 1000  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/007,520  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/327,357  
; FILING DATE:  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: CA 2,053,799-0  
; FILING DATE: 22-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ihnen, Jeffrey L.  
; REGISTRATION NUMBER: 28,957  
; REFERENCE/DOCKET NUMBER: 27052-115469  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-962-4810  
; TELEFAX: 202-962-8300  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 170 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; IMMEDIATE SOURCE:  
; CLONE: human myelin basic protein  
US-09-007-520-1

Query Match 100.0%; Score 103; DB 3; Length 170;  
Best Local Similarity 100.0%; Pred. No. 3.6e-10;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HYGSLPQKSHGRTQDENP 18  
|||||

Db 68 HYGSLPQKSHGRTQDENP 85

## RESULT 3

US-09-055-263-1  
; Sequence 1, Application US/09055263  
; Patent No. 6252040  
; GENERAL INFORMATION:  
; APPLICANT: WARREN, Kenneth G.  
; APPLICANT: CATZ, Ingrid  
; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC  
; TITLE OF INVENTION: PROTEIN AND THE ADMINISTRATION OF MYELIN BASIC PROTEIN  
; TITLE OF INVENTION: PEPTIDES TO MULTIPLE SCLEROSIS PATIENTS  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
; STREET: 1201 New York Avenue, N.W., Suite 1000  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/055,263  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/327,357  
; FILING DATE: 21-OCT-1994  
; APPLICATION NUMBER: US 07/798,099  
; FILING DATE: 27-NOV-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: CA 2,053,799-0  
; FILING DATE: 22-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ihnen, Jeffrey L.  
; REGISTRATION NUMBER: 28,957  
; REFERENCE/DOCKET NUMBER: 27052-115469  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-962-4810  
; TELEFAX: 202-962-8300  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 170 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; IMMEDIATE SOURCE:  
; CLONE: human myelin basic protein  
US-09-055-263-1

Query Match 100.0%; Score 103; DB 4; Length 170;  
Best Local Similarity 100.0%; Pred. No. 3.6e-10;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HYGSLPQKSHGRTQDENP 18  
|||||

Db 68 HYGSLPQKSHGRTQDENP 85

## RESULT 4

US-09-007-520-1  
; Sequence 1, Application US/09007520  
; Patent No. 6258781  
; GENERAL INFORMATION:

APPLICANT: WARREN, Kenneth G.  
CATZ, Ingrid  
TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC  
PROTEIN AND THE ADMINISTRATION OF MYELIN BASIC PROTEIN  
PEPTIDES TO MULTIPLE SCLEROSIS PATIENTS  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue, N.W., Suite 1000  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/09/007,520  
APPLICATION NUMBER: US/09/007,520  
FILING DATE: 15-Jan-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/327,357  
FILING DATE: <Unknown>  
APPLICATION NUMBER: CA 2,053,799-0  
FILING DATE: 22-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Innen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 27052-115469  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 170 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: human myelin basic protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-007-520-1

Query Match 100.0%; Score 103; DB 4; Length 170;  
Best Local Similarity 100.0%; Pred. No. 3.6e-10;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HYGSLPKSHGRTQDENP 18  
DB 68 HYGSLPKSHGRTQDENP 85  
RESULT 5  
US-08-342-408B-2  
Sequence 2, Application US/08342408B  
Patent No. 6329499  
GENERAL INFORMATION:  
APPLICANT: Ling, Nicholas  
APPLICANT: Gaur, Amitabh  
APPLICANT: Conlon, Paul J.  
APPLICANT: Steinman, Lawrence  
TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE  
SCLEROSIS USING PEPTIDE ANALOGUES OF HUMAN MYELIN BASIC  
PROTEIN  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/342,408B  
APPLICATION NUMBER: US/08/342,408B  
FILING DATE: 18-NOV-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6329499tenburg, Carol  
REGISTRATION NUMBER: 39,317  
REFERENCE/DOCKET NUMBER: 690068.405  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 170 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-342-408B-2

Query Match 100.0%; Score 103; DB 4; Length 170;  
Best Local Similarity 100.0%; Pred. No. 3.6e-10;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HYGSLPKSHGRTQDENP 18  
DB 68 HYGSLPKSHGRTQDENP 85

RESULT 6  
US-08-781-122-2  
Sequence 2, Application US/08781122  
Patent No. 5948764  
GENERAL INFORMATION:  
APPLICANT: Gaur, Amitabh  
APPLICANT: Conlon, Paul J.  
APPLICANT: Ling, Nicholas  
TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS  
UTILIZING PEPTIDE ANALOGUES OF HUMAN MYELIN BASIC PROTEIN  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/781,122  
APPLICATION NUMBER: US/08/781,122  
FILING DATE: 09-JAN-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 690068.418C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 171 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-781-122-2

Query Match 100.0%; Score 103; DB 2; Length 171;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18  
 Db 69 HYGSLPQKSHGRTQDENP 86  
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RESULT 7  
 US-09-137-759-2  
 ; Sequence 2, Application US/09137759  
 ; Patent No. 6251396  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaur, Amitabh  
 ; APPLICANT: Conlon, Paul J.  
 ; APPLICANT: Ling, Nicholas C.  
 ; APPLICANT: Staehlin, Theophil  
 ; APPLICANT: Crowe, Paul D.  
 ; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING  
 ; FILE REFERENCE: 630068.405C1  
 ; CURRENT APPLICATION NUMBER: US/09/137,759  
 ; CURRENT FILING DATE: 1998-08-20  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 2  
 ; LENGTH: 171  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-137-759-2

Query Match 100.0%; Score 103; DB 4; Length 171;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18  
 Db 69 HYGSLPQKSHGRTQDENP 86  
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RESULT 8  
 5194425-4  
 ; Patent No. 5194425  
 ; APPLICANT: SHARMA, SOMESH D.; LERCH, L. BERNARD; CLARK,  
 ; BRIAN R.  
 ; TITLE OF INVENTION: MHC-MEDIATED TOXIC CONJUGATES USEFUL IN  
 ; AMELIORATING AUTOIMMUNITY  
 ; NUMBER OF SEQUENCES: 9  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/367,751  
 ; FILING DATE: 21-JUN-1989  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 210,594  
 ; FILING DATE: 23-JUN-1988  
 ; SEQ ID NO: 4  
 ; LENGTH: 168  
 ; 5194425-4

Query Match 82.5%; Score 85; DB 6; Length 168;  
 Best Local Similarity 88.9%; Pred. No. 4.1e-07;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18  
 Db 66 HYGSLPQKSHGRTQDENP 83  
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RESULT 9  
 US-08-297-395-21  
 ; Sequence 21, Application US/08297395A  
 ; Patent No. 6039947  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Howard L. Weiner  
 ; APPLICANT: David A. Hafler  
 ; TITLE OF INVENTION: PEPTIDES DERIVED FROM IMMUNODOMINANT  
 ; FILE REFERENCE: 1010/05723US3  
 ; CURRENT APPLICATION NUMBER: US/08/297,395A  
 ; CURRENT FILING DATE: 1994-08-11  
 ; EARLIER APPLICATION NUMBER: 08/059,189  
 ; EARLIER FILING DATE: 1993-05-06  
 ; EARLIER APPLICATION NUMBER: 07/502,559  
 ; EARLIER FILING DATE: 1990-03-30  
 ; EARLIER APPLICATION NUMBER: PCT/US88/02139  
 ; EARLIER FILING DATE: 1988-06-24  
 ; EARLIER APPLICATION NUMBER: 07/065,734  
 ; EARLIER FILING DATE: 1987-06-24  
 ; NUMBER OF SEQ ID NOS: 84  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 21  
 ; LENGTH: 20  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-08-297-395-21

Query Match 79.6%; Score 82; DB 3; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SLPOKSHGRTQDENP 18  
 Db 1 SLPOKSHGRTQDENP 15  
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RESULT 10  
 US-08-297-395-2  
 ; Sequence 2, Application US/08297395A  
 ; Patent No. 6039947  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Howard L. Weiner  
 ; APPLICANT: David A. Hafler  
 ; TITLE OF INVENTION: PEPTIDES DERIVED FROM IMMUNODOMINANT  
 ; FILE REFERENCE: 1010/05723US3  
 ; CURRENT APPLICATION NUMBER: US/08/297,395A  
 ; CURRENT FILING DATE: 1994-08-11  
 ; EARLIER APPLICATION NUMBER: 08/059,189  
 ; EARLIER FILING DATE: 1993-05-06  
 ; EARLIER APPLICATION NUMBER: 07/502,559  
 ; EARLIER FILING DATE: 1990-03-30  
 ; EARLIER APPLICATION NUMBER: PCT/US88/02139  
 ; EARLIER FILING DATE: 1988-06-24  
 ; EARLIER APPLICATION NUMBER: 07/065,734  
 ; NUMBER OF SEQ ID NOS: 84  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 40  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-08-297-395-2

Query Match 79.6%; Score 82; DB 3; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 SLPOKSHGRTDQNP 18  
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 DB 1 SLPOKSHGRTDQNP 15

RESULT 11  
 US-08-227-372-1  
 ; Sequence 1, Application US/08227372  
 ; Patent No. 5763585  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nag, Bishwalit  
 ; TITLE OF INVENTION: PURIFICATION AND CHARACTERIZATION OF  
 ; MHC-PEPTIDE COMPLEXES USEFUL IN AMELIORATING AUTOIMMUNITY  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend Kourtie and Crew  
 ; STREET: Steuart Street Tower, One Market Plaza  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: US  
 ; ZIP: 94105-1493  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION NUMBER: US/08/227,372  
 ; FILING DATE: 14-APR-1994  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/136,216  
 ; FILING DATE: 13-OCT-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Bastian, Kevin L.  
 ; REGISTRATION NUMBER: 34,774  
 ; REFERENCE/DOCKET NUMBER: 14058-32-1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 543-9600  
 ; TELEFAX: (415) 543-5043  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 170 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: protein  
 ; FEATURE:  
 ; NAME/KEY: Protein  
 ; LOCATION: 1..170  
 ; OTHER INFORMATION: /note= "Myelin basic protein"  
 ; US-08-227-372-1

Query Match 73.3%; Score 75.5; DB 1; Length 170;  
 Best Local Similarity 78.9%; Pred. No. 1.7e-05;  
 Matches 15; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

OY 1 HYGSLPQKSHG-RTQDQNP 18  
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 DB 67 HYGSLPQKAGHRPDQNP 85

RESULT 12  
 US-08-462-351-3  
 ; Sequence 3, Application US/08462351  
 ; Patent No. 6106840  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sharma, Somesh D.  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME/KEY: Clark, Brian R.

APPLICANT: Lerch, Bernard L.  
 TITLE OF INVENTION: MHC Conjugates Useful in Ameliorating  
 TITLE OF INVENTION: Autoimmunity  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-3834  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA: US/08/462,351  
 APPLICATION NUMBER: US/08/462,351  
 FILING DATE: 05-JUN-1995  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/210,594  
 FILING DATE: 23-JUN-1988  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/576,084  
 FILING DATE: 30-AUG-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/690,840  
 FILING DATE: 23-APR-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/869,293  
 FILING DATE: 14-APR-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Parent, Annette S.  
 REGISTRATION NUMBER: 42,058  
 REFERENCE/DOCKET NUMBER: 014058-0002420S  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 170 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FEATURE:  
 NAME/KEY: Protein  
 LOCATION: 1..170  
 OTHER INFORMATION: /note= "myelin basic protein (MBP)"  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 1  
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 OTHER INFORMATION: /note= "Xaa = N-acetyl-alanine"  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 3  
 OTHER INFORMATION: /product= "OTHER"  
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 OTHER INFORMATION: or absent"  
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 NAME/KEY: Modified-site  
 LOCATION: 10  
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 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 11  
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 OTHER INFORMATION: /note= "Xaa = Ser or Gly"  
 FEATURE:  
 NAME/KEY: Modified-site

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; LOCATION: 16
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; NAME/KEY: Modified-site
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; US-08-462-351-3

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Query Match 73.3%; Score 75.5; DB 3; Length 170;
Best Local Similarity 78.9%; Pred. No. 1.7e-05;
Matches 15; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 HYGSLPQKSHG-RTQDENP 18
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Db 67 HYGSLPQKXGHRXQDENP 85

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RESULT 13
5194425-3

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; Patent No. 5194425
; APPLICANT: SHARMA, SOMESH D.; LERCH, L. BERNARD; CLARK,
; BRIAN R.
; TITLE OF INVENTION: MHC-MEDIATED TOXIC CONJUGATES USEFUL IN
; AMELIORATING AUTOIMMUNITY
; CURRENT APPLICATION DATA:
; NUMBER OF SEQUENCES: 9
; APPLICATION NUMBER: US/07/367,751
; FILING DATE: 21-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 210,594
; FILING DATE: 23-JUN-1988
; SEQ ID NO: 3
; LENGTH: 170
; 5194425-3

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Query Match 73.3%; Score 75.5; DB 6; Length 170;
Best Local Similarity 78.9%; Pred. No. 1.7e-05;
Matches 15; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

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Qy 1 HYGSLPQKSHG-RTQDENP 18
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Db 67 HYGSLPQKXGHRXQDENP 85

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RESULT 14
5468481-3
; Patent No. 5468481
; APPLICANT: SHARMA, SOMESH D.; CLARK, BRIAN R.; LERCH, BERNARD L.
; TITLE OF INVENTION: MHC CLASS II-PEPTIDE CONJUGATES USEFUL
; IN AMELIORATING AUTOIMMUNITY
; CURRENT APPLICATION DATA:
; NUMBER OF SEQUENCES: 7
; APPLICATION NUMBER: US/07/869,293
; FILING DATE: 14-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 690,840
; FILING DATE: 23-APR-1991
; APPLICATION NUMBER: 576,084
; FILING DATE: 30-AUG-1990
; APPLICATION NUMBER: 210,594
; FILING DATE: 23-JUN-1988
; APPLICATION NUMBER: 635,840
; FILING DATE: 28-DEC-1998
; APPLICATION NUMBER: 367,751
; FILING DATE: 21-JUN-1989
; SEQ ID NO: 3
; LENGTH: 170
; 5468481-3

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Query Match 73.3%; Score 75.5; DB 6; Length 170;
Best Local Similarity 78.9%; Pred. No. 1.7e-05;
Matches 15; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Qy 1 HYGSLPQKSHG-RTQDENP 18
| | | | | | | | | | | | | | | |
Db 67 HYGSLPQKXGHRXQDENP 85

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RESULT 15
US-08-470-397-1
; Sequence 1, Application US/08470397
; Patent No. 6007820
; GENERAL INFORMATION:
; APPLICANT: Nag, Bishwajit
; TITLE OF INVENTION: Purification and Characterization of
; MHC-Peptide Complexes Useful in Ameliorating Autoimmunity
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th

```



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; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470.397
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136,216
; FILING DATE: 13-OCT-1993
; APPLICATION DATA: US 08/227,372
; FILING DATE: 14-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14058-32-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
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; LOCATION: 3
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; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 10
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; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
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; FEATURE:
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; FEATURE:
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; NAME/KEY: Modified-site
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; NAME/KEY: Modified-site
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; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 144
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; US-08-470-397-1

Query Match 72.3%; Score 74.5; DB 3; Length 170;
Best Local Similarity 78.9%; Pred. No. 2.5e-05;
Matches 15; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 HYGSLPQKSHG-RYQDENP 18
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DB 67 HYGSLPQKXXGHRXQDENP 85

Search completed: August 28, 2002, 16:35:30
Job time: 192 sec
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2002, 16:39:34 ; Search time 205.27 Seconds  
(without alignments)  
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Title: US-09-813-383-1\_COPY\_8\_25  
Perfect score: 103  
Sequence: 1 HYGSLPQKSHGRTQDENP 18

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 s

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24: /cgn2_6/ptodata/2/paa/US101_COMB.pcp: *
25: /cgn2_6/ptodata/2/paa/US101_COMB.pcp: *
26: /cgn2_6/ptodata/2/paa/US60_COMB.pcp: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match	Length				
1	103	100.0	46	22	US-09-813-383-1		Sequence 1, Appl1
2	103	100.0	108	21	US-09-760-443-1465		Sequence 1465, Ap
3	103	100.0	108	21	US-09-760-495-898		Sequence 898, App
4	103	100.0	136	21	US-09-760-443-1435		Sequence 1435, Ap
5	103	100.0	136	21	US-09-760-495-651		Sequence 651, App
6	103	100.0	167	3	US-07-987-751-3		Sequence 3, Appl1
7	103	100.0	168	3	US-07-987-751-4		Sequence 4, Appl1

8	103	100.0	170	3	US-07-798-009A-1	Sequence 1, Appl
9	103	100.0	170	6	US-08-241-246-B-1	Sequence 1, Appl
10	103	100.0	170	6	US-08-241-246B-1	Sequence 1, Appl
11	103	100.0	170	7	US-08-327-357-1	Sequence 1, Appl
12	103	100.0	170	7	US-08-328-224-5	Sequence 5, Appl
13	103	100.0	170	7	US-08-342-078-2	Sequence 2, Appl
14	103	100.0	170	8	US-08-404-228-1	Sequence 1, Appl
15	103	100.0	170	8	US-08-462-941A-1	Sequence 1, Appl
16	103	100.0	170	8	US-08-463-412-1	Sequence 1, Appl
17	103	100.0	170	8	US-08-463-456-1	Sequence 1, Appl
18	103	100.0	170	8	US-08-481-938-1	Sequence 1, Appl
19	103	100.0	170	24	US-10-015-540-2	Sequence 2, Appl
20	103	100.0	171	1	PCT-US00-06233-4	Sequence 4, Appl
21	103	100.0	171	7	US-08-342-078A-2	Sequence 2, Appl
22	103	100.0	171	8	US-08-484-409-2	Sequence 2, Appl
23	103	100.0	171	13	US-08-953-937-2	Sequence 2, Appl
24	103	100.0	171	16	US-09-218-277-12	Sequence 12, Appl
25	103	100.0	171	16	US-09-267-590-4	Sequence 12, Appl
26	103	100.0	171	17	US-09-314-161-12	Sequence 2, Appl
27	103	100.0	171	17	US-09-378-244-2	Sequence 2, Appl
28	103	100.0	171	22	US-09-893-348-12	Sequence 12, Appl
29	103	100.0	171	23	US-09-947-770-4	Sequence 4, Appl
30	103	100.0	171	23	US-09-989-476-2	Sequence 2, Appl
31	103	100.0	171	24	US-10-000-439-12	Sequence 12, Appl
32	103	100.0	176	1	PCT-US01-14827-13007	Sequence 12, Appl
33	103	100.0	183	1	PCT-US01-08656-9330	Sequence 13007, A
34	103	100.0	186	17	US-09-310-707A-28	Sequence 9330, Ap
35	103	100.0	197	19	US-09-512-563-54	Sequence 28, Appl
36	103	100.0	197	19	US-09-512-563A-54	Sequence 54, Appl
37	103	100.0	197	19	US-09-512-563C-54	Sequence 54, Appl
38	103	100.0	203	18	US-09-463-186-1	Sequence 1, Appl
39	103	100.0	315	21	US-09-760-443-1502	Sequence 1502, Ap
40	103	100.0	315	21	US-09-760-446A-1779	Sequence 1779, Ap
41	103	100.0	325	1	PCT-US01-14827-13008	Sequence 13008, A
42	97	94.2	168	3	US-07-987-751-7	Sequence 7, Appl
43	95	92.2	170	3	US-07-798-099-1	Sequence 1, Appl
44	92.5	89.8	169	3	US-07-987-751-10	Sequence 10, Appl
45	88.5	85.9	166	26	US-60-196-710-5529	Sequence 5529, Ap

## ALIGNMENTS

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RESULT      1
US-09-813-383-1
; Sequence 1, Application US/09813383
; GENERAL INFORMATION:
;
; APPLICANT: WARREN, KENNETH G.
; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC PROTEIN AND
; TITLE OF INVENTION: THE ADMINISTRATION OF MYELIN BASIC PROTEIN PEPTIDES TO
; TITLE OF INVENTION: MULTIPLE SCLEROSIS PATIENTS
; FILE REFERENCE: 098810/027 8741
; CURRENT APPLICATION NUMBER: US/09/813,383
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; US-09-813-383-1

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Query Match	100.0%	Score 103;	DB 22;	Length 46;
Best Local Similarity	100.0%	Pred. No. 4.	le-09;	
Matches 18;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	HYGSLPKQKHGRQTQDENP	18	
Dd	8	HYGSLPKQKHGRQTQDENP	25	

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RESULT      2
US-09-760-443-1465
; Sequence 1465, Application US/09760443
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ212
; CURRENT APPLICATION NUMBER: US/09/760,443
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2164
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1465
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-443-1465

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Query Match      100.0%; Score 103; DB 21; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
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Db 18 HYGSLPQKSHGRTQDENP 35

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RESULT      3
US-09-760-495-898
; Sequence 898, Application US/09760495
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC021
; CURRENT APPLICATION NUMBER: US/09/760,495
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1064
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 898
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-495-898

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```

Query Match      100.0%; Score 103; DB 21; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
   |||||
Db 18 HYGSLPQKSHGRTQDENP 35

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RESULT      4
US-09-760-443-1435
; Sequence 1435, Application US/09760443
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ212
; CURRENT APPLICATION NUMBER: US/09/760,443
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2164
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1435
; LENGTH: 136
; TYPE: PRT

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (113)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (116)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (117)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (124)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (127)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (136)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-760-443-1435

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Query Match      100.0%; Score 103; DB 21; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
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Db 95 HYGSLPQKSHGRTQDENP 112

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RESULT      5
US-09-760-495-651
; Sequence 651, Application US/09760495
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC021
; CURRENT APPLICATION NUMBER: US/09/760,495
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1064
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 651
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (113)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (116)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (117)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (124)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (127)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (136)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-760-495-651

```

```

Query Match      100.0%; Score 103; DB 21; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HYGSLPKSHGRTQDENP 18  
 |||||  
 Db 95 HYGSLPKSHGRTQDENP 112

## RESULT 6

US-07-987-751-3  
 ; Sequence 3, Application US/07987751  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Clark, Brian R.  
 ; TITLE OF INVENTION: Methods for the Rapid Determination of  
 ; TITLE OF INVENTION: Antigen-Specific T Cell Frequency  
 ; NUMBER OF SEQUENCES: 12  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend Kourie and Crew  
 ; STREET: One Market Plaza, Steuart Tower, Suite 2000  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94105  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/987,751  
 ; FILING DATE: 19921204  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Smith, William M.  
 ; REGISTRATION NUMBER: 30,223  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-326-2400  
 ; TELEFAX: 415-326-2422  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 167 amino acids  
 ; TYPE: AMINO ACID  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-07-987-751-3

Query Match 100.0%; Score 103; DB 3; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPKSHGRTQDENP 18  
 |||||  
 Db 68 HYGSLPKSHGRTQDENP 85

## RESULT 7

US-07-987-751-4  
 ; Sequence 4, Application US/07987751  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Clark, Brian R.  
 ; TITLE OF INVENTION: Methods for the Rapid Determination of  
 ; TITLE OF INVENTION: Antigen-Specific T Cell Frequency  
 ; NUMBER OF SEQUENCES: 12  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend Kourie and Crew  
 ; STREET: One Market Plaza, Steuart Tower, Suite 2000  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94105  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/987,751  
 ; FILING DATE: 19921204  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Smith, William M.  
 ; REGISTRATION NUMBER: 30,223  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-326-2400  
 ; TELEFAX: 415-326-2422  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 168 amino acids  
 ; TYPE: AMINO ACID  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-07-987-751-4

Query Match 100.0%; Score 103; DB 3; Length 168;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPKSHGRTQDENP 18  
 |||||  
 Db 68 HYGSLPKSHGRTQDENP 85

## RESULT 8

US-07-798-099A-1  
 ; Sequence 1, Application US/07798099A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WARREN, Kenneth G.  
 ; APPLICANT: CATZ, Ingrid  
 ; TITLE OF INVENTION: SYNTHETIC PEPTIDE SPECIFICITY OF  
 ; TITLE OF INVENTION: ANTI-MYELIN BASIC PROTEIN FROM MULTIPLE SCLEROSIS  
 ; NUMBER OF SEQUENCES: 1  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Robert M. Phipps  
 ; STREET: 329 S. 9th Street  
 ; CITY: Mayfield  
 ; STATE: Kentucky  
 ; COUNTRY: USA  
 ; ZIP: 42066  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/798,099A  
 ; FILING DATE: 27-NOV-1991  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: CA 2,053,799-0  
 ; FILING DATE: 22-OCT-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: PHIPPS, Robert M.  
 ; REGISTRATION NUMBER: 20,959  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (502)247-9019  
 ; TELEFAX: (502)247-9019  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 170 amino acids

; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: homo sapien  
 ; IMMEDIATE SOURCE:  
 ; CLONE: human myelin basic protein  
 US-07-798-099A-1

Query Match 100.0%; Score 103; DB 3; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 2e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18  
 Db 68 HYGSLPQKSHGRTQDENP 85

RESULT 9  
 US-08-241-246-1  
 ; Sequence 1, Application US/08241246  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Smilek, Dawn;  
 ; APPLICANT: Hsu, Di-Hwei; and  
 ; APPLICANT: Shi, Jia-Dong.  
 ; TITLE OF INVENTION: COMPOSITIONS AND TREATMENT FOR MULTIPLE  
 ; NUMBER OF SEQUENCES: 1  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: LAHIVE & COCKFIELD  
 ; STREET: 60 State Street, suite 510  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: ASCII-text  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/241,246  
 ; FILING DATE: 10-MAY-1994  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/006,116  
 ; FILING DATE: 15-JANUARY-1993  
 ; REGISTRATION NUMBER: 36,207  
 ; REFERENCE/DOCKET NUMBER: IMI-053 (084.0US)  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (617) 227-7400  
 ; TELEFAX: (617) 227-5941  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 170 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-241-246-1

Query Match 100.0%; Score 103; DB 6; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 2e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18  
 Db 68 HYGSLPQKSHGRTQDENP 85

Query Match 100.0%; Score 103; DB 6; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 2e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HYGSLPQKSHGRTQDENP 18  
 Db 68 HYGSLPQKSHGRTQDENP 85

RESULT 10  
 US-08-241-246B-1  
 ; Sequence 1, Application US/08241246B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Smilek, Dawn; Hsu, Di-Hwei; and Shi, Jia-Dong  
 ; TITLE OF INVENTION: COMPOSITIONS AND TREATMENT FOR  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
 ; STREET: 28 State Street  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: ASCII-text  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/241,246B  
 ; FILING DATE: 10-MAY-1994  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/006,116  
 ; FILING DATE: 15-JANUARY-1993  
 ; REGISTRATION NUMBER: 36,207  
 ; REFERENCE/DOCKET NUMBER: IMI-053 (084.0US)  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (617) 227-7400  
 ; TELEFAX: (617) 742-4214  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 170 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; FRAGMENT TYPE: internal  
 US-08-241-246B-1

Query Match 100.0%; Score 103; DB 6; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 2e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18  
 Db 68 HYGSLPQKSHGRTQDENP 85

Query Match 100.0%; Score 103; DB 6; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 2e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18  
 Db 68 HYGSLPQKSHGRTQDENP 85

RESULT 11  
 US-08-327-357-1  
 ; Sequence 1, Application US/08327357  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WARREN, Kenneth G.  
 ; APPLICANT: CATZ, Ingrid  
 ; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN  
 ; NUMBER OF SEQUENCES: 1  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
 ; STREET: 1201 New York Avenue, N.W.

```

; CITY: Washington, D.C.
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3917
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,357
; FILING DATE: 21-OCT-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CA 2,053,799-0
; FILING DATE: 22-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Jeffrey L. Ihnen
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 18760-95536(temp)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)962-4800
; TELEFAX: (202)962-8300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; IMMEDIATE SOURCE:
; CLONE: human myelin basic protein
; US-08-327-357-1

```

```

Query Match 100.0%; Score 103; DB 7; Length 170;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HYGSLPKSHGRTQDENP 18
| | | | | | | | | | | | | | | | | |
DB 68 HYGSLPKSHGRTQDENP 85

```

```

RESULT 12
US-08-328-224-5
; Sequence 5, Application US/08328224
; GENERAL INFORMATION:
; APPLICANT: Smilek, Dawn
; APPLICANT: Samson, Michael
; APPLICANT: Geffer, Malcolm
; APPLICANT: Hsu, Di-Hwei
; APPLICANT: Shi, Jia-Doug
; APPLICANT: Paliard, Xavier
; APPLICANT: Devaux, Brigitte
; APPLICANT: Rothbard, Jonathan
; APPLICANT: Franzen, Henry M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ADMINISTERING TO HUMANS SUFFERIN
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,224
; FILING DATE: 10-25-94
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: 094.0 US (IMI-056)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
; US-08-328-224-5

```

```

Query Match 100.0%; Score 103; DB 7; Length 170;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HYGSLPKSHGRTQDENP 18
| | | | | | | | | | | | | | | | | |
DB 68 HYGSLPKSHGRTQDENP 85

```

```

RESULT 13
US-08-342-078-2
; Sequence 2, Application US/08342078
; GENERAL INFORMATION:
; APPLICANT: Steinman, Lawrence
; APPLICANT: Ling, Nicholas
; APPLICANT: Conlon, Paul J.
; APPLICANT: Gaur, Amitabh
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE
; TITLE OF INVENTION: SCLEROSIS USING PEPTIDE ANALOGUES AT POSITION 91 OF HUMAN
; TITLE OF INVENTION: MYELIN BASIC PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/342,078
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Nottenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 690068.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANDBERRY
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-342-078-2

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Query Match 100.0%; Score 103; DB 7; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 2e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPKSHGRTQDENP 18  
 |||||

Db 68 HYGSLPKSHGRTQDENP 85

## RESULT 14

US-08-404-228-1

; Sequence 1, Application US/08404228

; GENERAL INFORMATION:

; APPLICANT: Smilek, Dawn;

; APPLICANT: Samson, Michael F.;

; APPLICANT: Geffer, Malcolm;

; APPLICANT: Hsu, Di-Hwei;

; APPLICANT: Shi, Jia-Dong;

; APPLICANT: Pallard, Xavier;

; APPLICANT: Devaux, Brigitte;

; APPLICANT: Rothbard, Jonathan; and

; APPLICANT: Franzen, Henry M.

; TITLE OF INVENTION: Compositions and Treatment for Multiple

; NUMBER OF SEQUENCES: 71

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, Suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/404,228

; FILING DATE: 15-March-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Anne I. Craig

; REGISTRATION NUMBER: Reg. No. 32, 976

; REFERENCE/DOCKET NUMBER: 094.1 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 466-6000

; TELEFAX: (617) 466-6010

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 170 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal

US-08-404-228-1

Query Match 100.0%; Score 103; DB 8; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 2e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPKSHGRTQDENP 18  
 |||||

Db 68 HYGSLPKSHGRTQDENP 85

## RESULT 15

US-08-462-941A-1

; Sequence 1, Application US/08462941A

; GENERAL INFORMATION:

; APPLICANT: Smilek, Dawn;

; APPLICANT: Samson, Michael F.;

; APPLICANT: Geffer, Malcolm;

; APPLICANT: Hsu, Di-Hwei;

; APPLICANT: Shi, Jia-Dong;

; APPLICANT: Pallard, Xavier;

; APPLICANT: Devaux, Brigitte;

; APPLICANT: Rothbard, Jonathan; and

; APPLICANT: Franzen, Henry M.

; TITLE OF INVENTION: Compositions and Treatment for Multiple

; NUMBER OF SEQUENCES: 71

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, Suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/462,941A

; FILING DATE: 5-June-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/404,228

; FILING DATE: 15-March-1995

; APPLICATION NUMBER: US 08/328,224

; FILING DATE: 25-October-1994

; APPLICATION NUMBER: US 08/300,811

; FILING DATE: 1-September-1994

; APPLICATION NUMBER: US 08/241,246

; FILING DATE: 10-May-1994

; APPLICATION NUMBER: US 08/116,824

; FILING DATE: 3-September-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Amy E. Mandragouras

; REGISTRATION NUMBER: Reg. No. 36,207

; REFERENCE/DOCKET NUMBER: 094.1 USD1 (IMI-052CPDV)

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 170 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal

US-08-462-941A-1

Query Match 100.0%; Score 103; DB 8; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 2e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPKSHGRTQDENP 18  
 |||||

Db 68 HYGSLPKSHGRTQDENP 85

Search completed: August 28, 2002, 16:39:34  
 Job time: 346 sec







GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 28, 2002, 16:40:33 ; Search time 53.03 Seconds  
(without alignments)  
82.159 Million cell updates/sec

Title: US-09-813-383-1\_COPY\_8\_25  
Perfect score: 103  
Sequence: 1 HYGSLPKSHGRTQDENP 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747981 seqs, 242050750 residues

Total number of hits satisfying chosen parameters: 747981

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_New:\*

- 1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep.\*
- 7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	103	100.0	46	5	US-09-813-463A-1
2	103	100.0	108	6	US-10-143-775-898
3	103	100.0	108	6	US-10-212-054-1465
4	103	100.0	136	6	US-10-143-775-651
5	103	100.0	136	6	US-10-212-054-1435
6	103	100.0	171	1	PCT-US02-13527-12
7	103	100.0	171	6	US-10-104-973-2
8	103	100.0	172	4	US-08-431-644B-4
9	103	100.0	172	4	US-08-431-644C-4
10	103	100.0	197	4	US-08-431-644B-1
11	103	100.0	197	4	US-08-431-644C-1
12	103	100.0	203	4	US-08-431-644B-2
13	103	100.0	203	4	US-08-431-644B-3
14	103	100.0	203	4	US-08-431-644B-27
15	103	100.0	203	4	US-08-431-644C-2
16	103	100.0	203	4	US-08-431-644C-3
17	103	100.0	203	4	US-08-431-644C-27
18	103	100.0	315	6	US-10-206-664-1779
19	103	100.0	315	6	US-10-212-054-1502
20	82	79.6	315	5	US-09-813-463A-6
21	67	65.0	20	5	US-09-906-206A-34
22	67	65.0	20	5	US-09-715-708A-35
23	66.5	64.6	17	1	PCT-US02-00337-1
24	64	62.1	15	5	US-09-813-463A-4
25	63.5	61.7	19	1	PCT-US02-13873-30
26	62	60.2	21	5	US-09-813-463A-3

27	59.5	57.8	19	1	PCT-US02-13873-25	Sequence 25, Appli
28	49.5	48.1	37	1	PCT-US02-13873-4	Sequence 4, Appli
29	47.5	46.1	987	5	US-09-935-625-6080	Sequence 6080, Ap
30	47.5	46.1	987	5	US-09-935-625-14260	Sequence 14260, A
31	47.5	46.1	987	5	US-09-935-625-23047	Sequence 23047, A
32	47.5	46.1	987	5	US-09-935-625-26918	Sequence 26918, A
33	47.5	46.1	994	5	US-09-935-625-6079	Sequence 6079, Ap
34	47.5	46.1	994	5	US-09-935-625-14259	Sequence 14259, A
35	47.5	46.1	994	5	US-09-935-625-23046	Sequence 23046, A
36	47.5	46.1	994	5	US-09-935-625-26917	Sequence 26917, A
37	47.5	46.1	1123	5	US-09-935-625-6078	Sequence 6078, Ap
38	47.5	46.1	1123	5	US-09-935-625-14258	Sequence 14258, A
39	47.5	46.1	1123	5	US-09-935-625-23045	Sequence 23045, A
40	47.5	46.1	1123	5	US-09-935-625-26916	Sequence 26916, A
41	46	44.7	15	5	US-09-813-463A-5	Sequence 5, Appli
42	46	44.7	230	7	US-60-360-039-2545	Sequence 2545, Ap
43	46	43.7	23	5	US-09-906-206A-8	Sequence 8, Appli
44	45	43.7	23	5	US-09-715-708A-1	Sequence 1, Appli
45	45	43.7	24	5	US-09-707-738-2	Sequence 2, Appli

## ALIGNMENTS

RESULT 1  
US-09-813-463A-1  
; Sequence 1, Application US/09813463A  
; GENERAL INFORMATION:  
; APPLICANT: WARREN, KENNETH G.  
; APPLICANT: CATZ, INGRID  
; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC PROTEIN AND  
; TITLE OF INVENTION: THE ADMINISTRATION OF MYELIN BASIC PROTEIN PEPTIDES TO  
; TITLE OF INVENTION: MULTIPLE SCLEROSIS PATIENTS  
; FILE REFERENCE: 098810/027 8740  
; CURRENT APPLICATION NUMBER: US/09/813,463A  
; CURRENT FILING DATE: 2002-01-11  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 46  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-813-463A-1

Query Match 100.0%; Score 103; DB 5; Length 46;  
Best Local Similarity 100.0%; Pred. No. 2.7e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPKSHGRTQDENP 18  
Db 8 HYGSLPKSHGRTQDENP 25

RESULT 2  
US-10-143-775-898  
; Sequence 898, Application US/10143775  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC021C1N  
; CURRENT APPLICATION NUMBER: US/10/143,775  
; CURRENT FILING DATE: 2002-05-14  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 1064  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 898  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-143-775-898

Query Match 100.0%; Score 103; DB 6; Length 108;  
Best Local Similarity 100.0%; Pred. No. 6.8e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18  
|||||

Db 18 HYGSLPQKSHGRTQDENP 35

RESULT 3

US-10-212-054-1465

; Sequence 1465, Application US/10212054  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PJ212C1N  
; CURRENT APPLICATION NUMBER: US/10/212,054  
; CURRENT FILING DATE: 2002-08-06  
; NUMBER OF SEQ ID NOS: 2164  
; Prior application removed - See File Wrapper or Palm  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1465  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-212-054-1465

Query Match 100.0%; Score 103; DB 6; Length 108;  
Best Local Similarity 100.0%; Pred. No. 6.8e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18  
|||||

Db 18 HYGSLPQKSHGRTQDENP 35

RESULT 4

US-10-143-775-651

; Sequence 651, Application US/10143775  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC021C1N  
; CURRENT APPLICATION NUMBER: US/10/143,775  
; CURRENT FILING DATE: 2002-05-14  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 1064  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 651  
; LENGTH: 136  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (113)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (116)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (117)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (124)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:

; NAME/KEY: misc\_feature  
; LOCATION: (127)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (136)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-10-143-775-651

Query Match 100.0%; Score 103; DB 6; Length 136;  
Best Local Similarity 100.0%; Pred. No. 8.8e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18  
|||||

Db 95 HYGSLPQKSHGRTQDENP 112

RESULT 5

US-10-212-054-1435

; Sequence 1435, Application US/10212054  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PJ212C1N  
; CURRENT APPLICATION NUMBER: US/10/212,054  
; CURRENT FILING DATE: 2002-08-06  
; NUMBER OF SEQ ID NOS: 2164  
; Prior application removed - See File Wrapper or Palm  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1435  
; LENGTH: 136  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (113)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (116)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (117)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (124)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (127)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (136)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-10-212-054-1435

Query Match 100.0%; Score 103; DB 6; Length 136;  
Best Local Similarity 100.0%; Pred. No. 8.8e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18  
|||||

Db 95 HYGSLPQKSHGRTQDENP 112

RESULT 6

PCT-US02-13527-12

; Sequence 12, Application PCT/US0213527  
; GENERAL INFORMATION:  
; APPLICANT: Regents of the University of California  
; APPLICANT: Saxon, Andrew  
; APPLICANT: Zhang, Ke  
; APPLICANT: Zhu, Daocheng  
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR  
; TREATMENT OF IMMUNE DISEASES  
; FILE REFERENCE: UC067.004QPC  
; CURRENT APPLICATION NUMBER: PCT/US02/13527  
; PRIOR FILING DATE: 2002-05-01  
; PRIOR APPLICATION NUMBER: US 09/847,208  
; PRIOR FILING DATE: 2001-05-01  
; PRIOR APPLICATION NUMBER: US 10/000,439  
; PRIOR FILING DATE: 2001-10-24  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 171  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US02-13527-12

Query Match 100.0%; Score 103; DB 1; Length 171;  
Best Local Similarity 100.0%; Pred. No. 1.1e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPKSHGRTQDENP 18  
|||||  
Db 69 HYGSLPKSHGRTQDENP 86

## RESULT 7

US-10-104-973-2  
; Sequence 2, Application US/10104973  
; GENERAL INFORMATION:

; APPLICANT: Gaur, Amitabh  
; APPLICANT: Conlon, Paul J.  
; APPLICANT: Ling, Nicholas C.  
; APPLICANT: Staehlin, Theophil  
; APPLICANT: Crowe, Paul D.  
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING  
; TITLE OF INVENTION: PEPTIDE ANALOGS OF HUMAN MYELIN BASIC PROTEIN  
; FILE REFERENCE: 690068.405C4  
; CURRENT APPLICATION NUMBER: US/10/104,973  
; CURRENT FILING DATE: 2002-03-20  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 171  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-104-973-2

Query Match 100.0%; Score 103; DB 6; Length 171;  
Best Local Similarity 100.0%; Pred. No. 1.1e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPKSHGRTQDENP 18  
|||||  
Db 69 HYGSLPKSHGRTQDENP 86

## RESULT 8

US-08-431-644B-4  
; Sequence 4, Application US/08431644B  
; GENERAL INFORMATION:

; APPLICANT: Nye, Steven H.  
; APPLICANT: Lenardo, Michael J.  
; APPLICANT: McFarland, Henry F.  
; APPLICANT: Matis, Louis A.

; APPLICANT: Mueller, Eileen E.  
; APPLICANT: Mueller, John P.  
; APPLICANT: Pelfrey, Clara M.  
; APPLICANT: Squinto, Stephen P.  
; APPLICANT: Wilkins, James A.  
; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES  
; FILE REFERENCE: 1087-48(27)  
; CURRENT APPLICATION NUMBER: US/08/431,644B  
; CURRENT FILING DATE: 1995-05-02  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 172  
; TYPE: PRT  
; ORGANISM: human  
US-08-431-644B-4

Query Match 100.0%; Score 103; DB 4; Length 172;  
Best Local Similarity 100.0%; Pred. No. 1.1e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPKSHGRTQDENP 18  
|||||  
Db 70 HYGSLPKSHGRTQDENP 87

## RESULT 9

US-08-431-644C-4  
; Sequence 4, Application US/08431644C  
; GENERAL INFORMATION:

; APPLICANT: Nye, Steven H.  
; APPLICANT: Lenardo, Michael J.  
; APPLICANT: McFarland, Henry F.  
; APPLICANT: Matis, Louis A.  
; APPLICANT: Mueller, Eileen E.  
; APPLICANT: Mueller, John P.  
; APPLICANT: Pelfrey, Clara M.  
; APPLICANT: Squinto, Stephen P.  
; APPLICANT: Wilkins, James A.  
; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES  
; FILE REFERENCE: 1087-48(27)  
; CURRENT APPLICATION NUMBER: US/08/431,644C  
; CURRENT FILING DATE: 1995-05-02  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 172  
; TYPE: PRT  
; ORGANISM: human  
US-08-431-644C-4

Query Match 100.0%; Score 103; DB 4; Length 172;  
Best Local Similarity 100.0%; Pred. No. 1.1e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPKSHGRTQDENP 18  
|||||  
Db 70 HYGSLPKSHGRTQDENP 87

## RESULT 10

US-08-431-644B-1  
; Sequence 1, Application US/08431644B  
; GENERAL INFORMATION:

; APPLICANT: Nye, Steven H.  
; APPLICANT: Lenardo, Michael J.  
; APPLICANT: McFarland, Henry F.  
; APPLICANT: Matis, Louis A.  
; APPLICANT: Mueller, Eileen E.  
; APPLICANT: Mueller, John P.  
; APPLICANT: Pelfrey, Clara M.

```

; APPLICANT: Squinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES
; FILE REFERENCE: 1087-48(27)
; CURRENT APPLICATION NUMBER: US/08/431.644B
; CURRENT FILING DATE: 1995-05-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 197
; TYPE: PRT
; ORGANISM: human
US-08-431-644B-1

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Query Match	100.0%	Score 103;	DB 4;	Length 197;
Best Local Similarity	100.0%;	Pred. No. 1.3e-08;		
Matches 18;	Conservative	0;	Mismatches	0; Indels
QY	1	HYGSLPKQSHGRQTDPEN	18	
Db	95	HYGSLPKQSHGRQTDPEN	112	

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RESULT      11
US-08-431-644C-1
? SEQUENCE 1, Application US/08431644C
?
? GENERAL INFORMATION:
?
? APPLICANT: Nye, Steven H.
? APPLICANT: Lenardo, Michael J.
? APPLICANT: McFarland, Henry F.
? APPLICANT: Matis, Louis A.
? APPLICANT: Mueller, Eileen E.
? APPLICANT: Mueller, John P.
? APPLICANT: Pelfrey, Clara M.
? APPLICANT: Squinto, Stephen P.
? APPLICANT: Wilkins, James A.
?
? TITLE OF INVENTION: MODIFIED MYELIN
?
? FILE REFERENCE: 1087-48(27)
?
? CURRENT APPLICATION NUMBER: US/08/431-644C-1
?
? NUMBER FILING DATE: 1995-05-02
?
? NUMBER OF SEQ ID NOS: 27
?
? SOFTWARE: PatentIn version 3.1
?
? SEQ ID NO 1
?
? LENGTH: 197
?
? TYPE: PRT
?
? ORGANISM: human
?
US-08-431-644C-1

```

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Query Match      100.0%; Score 103; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels

QY 1 HYGSLPQKSHGRGTQDENP 18
   |||
DB 95 HYGSLPQKSHGRGTQDENP 112
   |||

```

```

RESULT 12
US-08-431-6448-2
; Sequence 2, Application US/08431644B
; GENERAL INFORMATION:
; APPLICANT: Nye, Steven H.
; APPLICANT: Lenardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matis, Louis A.
; APPLICANT: Mueller, Eileen E.
; APPLICANT: Mueller, John P.
; APPLICANT: Peifrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: MODIFIED MYELIN

```

```

; FILE REFERENCE: 1087-48(27)
; CURRENT APPLICATION NUMBER: US/08/431.644B
; CURRENT FILING DATE: 1995-05-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 203
; TYPE: PRT
; ORGANISM: human
US-08-431-644B-2

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Query Match	100.0%	Score 103;	DB 4;	Length 203;
Best Local Similarity	100.0%;	Pred. No. 1.4e-08;		
Matches 18; Conservative	0;	Mismatches	0;	Indels
Qy	1	HYGSLPKSHGRTQDENP	18	
Db	95	HYGSLPKSHGRTQDENP	112	

```

RESULT 13
US-08-431-644B-3
; Sequence 3, Application US/08431644B
; GENERAL INFORMATION:
; APPLICANT: Nye, Steven H.
; APPLICANT: Lenardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matis, Louis A.
; APPLICANT: Mueller, Eileen E.
; APPLICANT: Mueller, John P.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES
; FILE REFERENCE: 1087-48(27)
; CURRENT APPLICATION NUMBER: US/08/431.644B
; CURRENT FILING DATE: 1995-05-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 203
; TYPE: PRT
; ORGANISM: human
; US-08-431-644B-3

```

```

Query Match      100.0%; Score 103; DB 4; Length 203;
Best local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYGSLPKSHGRTQDENP 18
         |||||
Db       95 HYGSLPKSHGRTQDENP 112

```

```

RESULT 14
US-08-431-644B-27
; Sequence 27, Application US/08431644B
; GENERAL INFORMATION:
; APPLICANT: Nye, Steven H.
; APPLICANT: Lenardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matis, Louis A.
; APPLICANT: Mueller, Eileen E.
; APPLICANT: Mueller, John P.
; APPLICANT: Peltfey, Clara M.
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Watkins, James A.
; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES
; FILE REFERENCE: 1087-48(27)
; CURRENT APPLICATION NUMBER: US/08/431.644B
; CURRENT FILING DATE: 1995-05-02

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Thu Aug 29 10:03:57 2002

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; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 203
; TYPE: PRT
; ORGANISM: human
US-08-431-644B-27
```

```
Query Match      100.0%   Score 103;   DB 4;   Length 203;
Best Local Similarity 100.0%;   Pred. No. 1.4e-08;
Matches 18;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;
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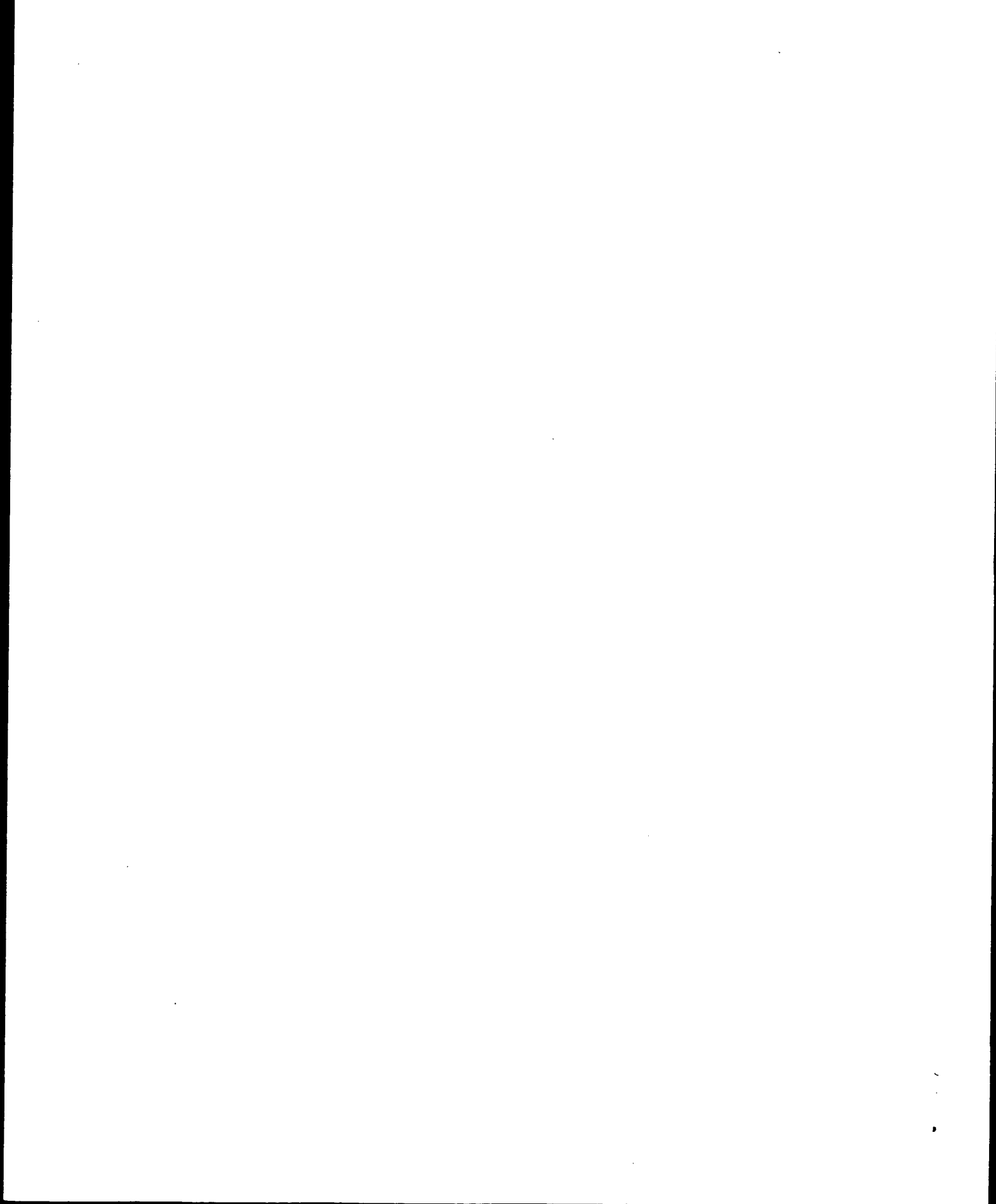
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QY 1 HYGSLPQKSHGRTQDENP 18
Db 95 HYGSLPQKSHGRTQDENP 112
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RESULT 15
US-08-431-644C-2
; Sequence 2. Application US/08431644C
; GENERAL INFORMATION:
; APPLICANT: Nye, Steven H.
; APPLICANT: Leonardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matis, Louis A.
; APPLICANT: Mueller, Eileen E.
; APPLICANT: Mueller, John P.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES
; FILE REFERENCE: 1087-48(27)
; CURRENT APPLICATION NUMBER: US/08/431.644C
; CURRENT FILING DATE: 1995-05-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 203
; TYPE: PRT
; ORGANISM: human
US-08-431-644C-2
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Query Match      100.0%   Score 103;   DB 4;   Length 203;
Best Local Similarity 100.0%;   Pred. No. 1.4e-08;
Matches 18;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;
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QY 1 HYGSLPQKSHGRTQDENP 18
Db 95 HYGSLPQKSHGRTQDENP 112
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Search completed: August 28, 2002, 16:40:34  
Job time: 386 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2002, 16:36:03 ; Search time 25.27 Seconds  
(without alignments)  
68.445 Million cell updates/sec

Title: US-09-813-383-1-copy\_8\_25

Perfect score: 103

Sequence: 1 HYGSLPKSHGRQTQDENP 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR.71.\*

1: PIR1.\*

2: PIR2.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	103	100.0	197	1 MBHUB	myelin basic prote
2	92.5	89.8	328	1 MBWSB	goli-myelin basic
3	85	82.5	171	1 MBGZB	myelin basic prote
4	83.5	81.1	171	1 MBPGB	myelin basic prote
5	76.7	76.7	128	2 B92087	myelin basic prote
6	78.5	76.2	128	1 MBRTS	myelin basic prote
7	75.5	73.3	169	1 MBBOB	myelin basic prote
8	74.5	72.3	167	2 A37246	myelin basic prote
9	63.5	61.7	174	2 S08535	myelin basic prote
10	48	46.6	393	2 T35894	hypothetical prote
11	46	44.7	230	2 S41043	ruml protein - fis
12	46	44.7	230	2 T40233	Rumlp - fission ye
13	46	44.7	257	2 D82350	Ribonuclease PH VC
14	46	44.7	632	2 F83387	copper resistance
15	45	43.7	238	1 A64059	tRNA nucleotidyltr
16	44	42.7	237	2 E90476	hypothetical prote
17	44	42.7	295	2 S58850	homeotic protein a
18	44	42.7	497	1 A29055	aldhyde dehydroge
19	43	41.7	366	2 JC7690	Gfi-1-like protein
20	42	40.8	241	2 C82673	Ribonuclease PH XF
21	42	40.8	316	2 D83233	hypothetical prote
22	42	40.8	491	2 A49179	melanoma antigen h
23	42	40.8	2531	2 T31070	notch homolog - se
24	41	39.8	115	2 T26191	hypothetical prote
25	41	39.8	168	2 A39316	RAB-17 protein - m
26	41	39.8	168	2 S08633	Ribosomal protein
27	41	39.8	205	2 F87560	plasmid replicatio
28	41	39.8	254	2 C82868	DNA-binding protei
29	41	39.8	340	2 F33282	

30	41	39.8	554	2 A91250	probable portal pr
31	41	39.8	932	2 S62555	protoplast regener
32	41	39.8	1180	1 NCECX5	exodeoxyribonuclea
33	41	39.8	1180	2 E91088	DNA helicase RecB
34	41	39.8	1180	2 G85933	DNA helicase RecB
35	41	39.8	1285	2 T14171	ataxin-2 - mouse
36	41	39.8	1909	2 A45592	liver stage antige
37	41	39.8	4957	2 T03455	ALR protein - huma
38	41	39.8	5262	2 T03454	ALR protein - huma
39	40.5	39.3	676	2 B72071	ribonuclease famil
40	40.5	39.3	676	2 D86553	ribonuclease famil
41	40	38.8	152	2 S72235	superoxide dismuta
42	40	38.8	188	1 R5XL8A	ribosomal protein
43	40	38.8	188	1 R5XL14	ribosomal protein
44	40	38.8	238	2 AE0006	tRNA nucleotidyltr
45	40	38.8	390	2 T46028	hypothetical prote

## ALIGNMENTS

RESULT 1

MBHUB

myelin basic protein [validated] - human

N:Contains: myelin basic protein precursor, 17.2K splice form; myelin basic protein p

.5K splice form

C:Species: Homo sapiens (man)

C:date: 18-Dec-1981 #sequence\_revision 25-Aug-1995 #text\_change 20-Apr-2001

C:Accession: S10482; A94106; B94106; A90256; JH0802; A60862; A61420; A33273; I54219;

R:Streicher, R.; Stoffel, W.

Biol. Chem. Hoppe-Seyler 370, 503-510, 1989

A:title: The organization of the human myelin basic protein gene. Comparison with the

A:Reference number: S10482; MUID:89302693

A:Accession: S10482

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-197 <SPR>

A:CROSS-references: EMBL:X17286; NID:g34490; PIDN:CAA35179.1; PID:g1184244

R:Kamholz, J.; De Ferra, F.; Puckett, C.; Lazzarini, R.

Proc. Natl. Acad. Sci. U.S.A. 83, 4962-4966, 1986

A:title: Identification of three forms of human myelin basic protein by cDNA cloning.

A:Reference number: A94106; MUID:86259714

A:Accession: A94106

A:Molecule type: mRNA

A:Residues: 1-59,86-197 <RAM>

A:CROSS-references: GB:M13577; NID:g187408; PIDN:AAA59562.1; PID:g307160

A>Note: 18.5K splice form

A:Accession: B94106

A:Molecule type: mRNA

A:Residues: 1-197 <KA2>

A>Note: antibody to the exon 2 encoded sequence detected a 21.5K splice form

A>Note: a 17.2K splice form is also described

A>Note: antibody to the exon 2 encoded sequence detected a 21.5K splice form; a 17.2K

R:Carnegele, P.R.

Biochem. J. 123, 57-67, 1971

A:title: Amino acid sequence of the encephalitogenic basic protein from human myelin.

A:Reference number: A90256; MUID:72066400

A:Accession: A90256

A:Molecule type: protein

A:Residues: 2-59,86-197 <CAR>

R:Proost, P.; Van Damme, J.; Opdenakker, G.

Biochem. Biophys. Res. Commun. 192, 1175-1181, 1993

A:title: Leukocyte gelatinase B cleavage releases encephalitogens from human myelin b

A:Reference number: JH0802; MUID:93282820

A:Accession: JH0802

A:Molecule type: protein

A:Residues: 2-59,86-197 <PRO>

A:Experimental source: brain

R:Scobie, H.A.; Whitaker, J.N.; Biemann, K.

J. Neurochem. 47, 614-616, 1986

A:title: Analysis of the primary sequence of human myelin basic protein peptides 1-44

A:Reference number: A60862; MUID:86280476

A:Accession: A60862

A:Molecule type: protein  
A:Residues: 2-45,117-197 <SCO>  
A:Note: evidence for acetylated amino end  
R:Gibson, B.W.; Gilliom, R.D.; Whitaker, J.N.; Biemann, K.  
J. Biol. Chem. 259, 5028-5031, 1984  
A:Title: Amino acid sequence of human myelin basic protein peptide 45-89 as determined by mass spectrometry  
A:Reference number: A61420; MUID:84185608  
A:Accession: A61420  
A:Molecule type: protein  
A:Residues: 46-59,86-116 <GIB>  
R:Wood, D.D.; Moscarello, M.A.  
J. Biol. Chem. 264, 5121-5127, 1989  
A:Title: The isolation, characterization, and lipid-aggregating properties of a citrulline-rich myelin basic protein peptide  
A:Reference number: A33273; MUID:89174797  
A:Accession: A33273  
A:Molecule type: protein  
A:Residues: 15-25,'X',27-31,'X',33-59,86-148,'X',150-156,'X',158-185,'X',187-196,'X' <WC>  
R:Baldwin, G.S.; Carnegie, P.R.  
Biochem. J. 123, 69-74, 1971  
A:Title: Isolation and partial characterization of methylated arginines from the encephalomyelinase-sensitive fraction of bovine myelin  
A:Reference number: A90257; MUID:72066401  
A:Contents: annotation; methylarginine  
A:Note: Arg-134 may be unmodified, monomethylarginine, or dimethylarginine in the approx 10% of the total arginine  
R:Lennon, V.A.; Wilks, A.V.; Carnegie, P.R.  
J. Immunol. 105, 1223-1230, 1970  
A:Reference number: A92806; MUID:71088405  
A:Contents: annotation  
A:Note: a region including residues 139-149 induces experimental autoimmune encephalomyelitis in mice  
R:Boylan, K.B.; Ayres, T.M.; Popko, B.; Takahashi, N.; Hood, L.E.; Prusiner, S.B.  
Genomics 6, 16-22, 1990  
A:Title: Repetitive DNA (CGG)n 5' to the human myelin basic protein gene: a new form of polyoma virus  
A:Reference number: I54219; MUID:90152679  
A:Accession: I54219  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-59 <RES>  
A:Cross-references: GB:M63599; NID:g187402; PIDN:AAA59560.1; PID:g187403  
R:Roth, H.J.; Kronquist, K.E.; Kerlero de Rosbo, N.; Crandall, B.F.; Campagnoni, A.T.  
J. Neurosci. Res. 17, 321-328, 1987  
A:Title: Evidence for the expression of four myelin basic protein variants in the developing mouse brain  
A:Reference number: I56567; MUID:87311781  
A:Accession: I56567  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-132,144-197 <RE2>  
A:Cross-references: GB:M30516; NID:g187410; PIDN:AAA59563.1; PID:g307161  
A:Accession: I73634  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-197 <RE3>  
A:Cross-references: GB:M30515; NID:g187412; PIDN:AAA59564.1; PID:g307162  
R:Roth, H.J.; Kronquist, K.; Pretorius, P.J.; Crandall, B.F.; Campagnoni, A.T.  
J. Neurosci. Res. 16, 227-238, 1986  
A:Title: Isolation and characterization of a cDNA coding for a novel human 17.3K myelin protein  
A:Reference number: I56565; MUID:86308101  
A:Accession: I56565  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-59,86-133,145-197 <RE4>  
A:Cross-references: GB:M30047; NID:g187400; PIDN:AAA59559.1; PID:g307159  
R:Boulias, C.; Pang, H.; Mastroratti, F.; Moscarello, M.A.  
Arch. Biochem. Biophys. 322, 174-182, 1995  
A:Title: The isolation and characterization of four myelin basic proteins from the unbound fraction of bovine myelin  
A:Reference number: S66383; MUID:96004793  
A:Accession: S66383  
A:Molecule type: protein  
A:Residues: 23-25,'X',27-39 <BOU>  
A:Comment: Four alternatively spliced forms of myelin basic protein have been observed, C, D, E, and F  
A:Gene: GDB:MBP  
A:Cross-references: GDB:I19379; OMIM:159430  
A:Map position: 18q22-18qter

A:Introns: 59/3; 85/3; 120/3; 132/3; 143/3; 183/3  
C:Function:  
A:Description: probably helps maintain myelin structure  
C:Superfamily: myelin basic protein  
C:Keywords: acetylated amino end; alternative splicing; citrulline; experimental auto  
F:2-132,144-197/Product: myelin basic protein, 21.5K splice form #status predicted <WAT>  
F:2-132,144-197/Product: myelin basic protein, 20.2K splice form #status experimental <M>  
F:2-59,86-132,144-197/Product: myelin basic protein, 18.5K splice form #status predicted  
F:2-59,86-132,144-197/Product: myelin basic protein, 17.2K splice form #status experimental  
F:2-59,86-132,144-197/Product: myelin basic protein, 17.2K splice form #status experimental  
F:26,32,149,157,186,197/Modified site: citrulline (Arg) (in form C-8) #status experimental  
F:134/Modified site: omega-N-methylarginine or omega-N,omega-N'-dimethylarginine (Arg)  
Query Match 100.0%; Score 103; DB 1; Length 197;  
Best Local Similarity 100.0%; Pred. No. 9,5e-10; Indels 0; Gaps 0;  
Matches 18; Conservative 0; Mismatches 0;  
QY 1 HYGSLPQKSHGRQTQDENP 18  
Db 95 HYGSLPQKSHGRQTQDENP 112  
|||||  
RESULT 2  
MBMSB  
golli-myelin basic protein precursor - mouse  
N:Alternate names: golli-mbp protein; MBP  
N:Contains: myelin basic protein  
C:Species: Mus musculus (house mouse)  
C>Date: 17-Mar-1987 #sequence\_revision 07-Oct-1994 #text\_change 22-Jun-1999  
R:Campagnoni, A.T.; Pribyl, T.M.; Campagnoni, C.W.; Kampf, K.; Amur-Umarjee, S.; Land  
J. Biol. Chem. 268, 4930-4938, 1993  
A:Title: Structure and developmental regulation of Golli-mbp, a 105-kilobase gene that encodes a family of myelin basic proteins  
A:Reference number: A45421; MUID:93186801  
A:Accession: A45421  
A:Molecule type: mRNA  
A:Residues: 1-190;217-276;316-328 <CAM1>  
A:Cross-references: GB:L07507; NID:g193584  
A:Experimental source: clone J37  
A:Note: sequence extracted from NCBI backbone (NCBIN:126696) and modified  
A:Accession: B45421  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-191,'SSEP' <CAM2>  
A:Cross-references: GB:L07508; NID:g193586; PIDN:AAA37721.1; PID:g193587  
A:Experimental source: clone BG21  
A:Note: sequence extracted from NCBI backbone (NCBIN:126700, NCBIP:126715)  
R:de Ferra, F.; Engh, H.; Hudson, L.; Kamholz, J.; Puckett, C.; Molineaux, S.; Lazzar  
Cell 43, 721-727, 1985  
A:Title: Alternative splicing accounts for the four forms of myelin basic protein.  
A:Reference number: A90875; MUID:86079555  
A:Accession: A90875  
A:Molecule type: mRNA  
A:Residues: 134-328 <DEF>  
A:Cross-references: GB:L00404; GB:M11669; NID:g199060; PIDN:AAA39502.1; PID:g387419  
A:Experimental source: 21.5K  
R:Takahashi, N.; Roach, A.; Teplow, D.B.; Prusiner, S.B.; Hood, L.  
Cell 42, 139-148, 1985  
A:Title: Cloning and characterization of the myelin basic protein gene from mouse: on  
A:Reference number: A90867; MUID:85254913  
A:Accession: A90867  
A:Molecule type: DNA  
A:Residues: 134-190;217-328 <TAK>  
A:Cross-references: GB:M11533; NID:g199044; PIDN:AAA39496.1; PID:g387414  
A:Experimental source: 18.5K  
R:Newman, S.; Kitamura, K.; Campagnoni, A.T.  
Proc. Natl. Acad. Sci. U.S.A. 84, 886-890, 1987  
A:Title: Identification of a cDNA coding for a fifth form of myelin basic protein in  
A:Reference number: A94188; MUID:87118269  
A:Accession: A26591  
A:Molecule type: mRNA

A:Residues: 134-274;316-328 <NEW1>  
A:Cross-references: GB:M15060; NID:g199048; PIDN:AA59711.1; PID:g199049  
A:Experimental source: clone M722; splice form 17.22K  
A:Accession: B26591  
A:Molecule type: mRNA  
A:Residues: 134-190;217-263;275-328 <NEW2>  
A:Cross-references: GB:M15062; NID:g199050  
A:Experimental source: clone M78; splice form 17.24K  
R:Kitamura, K.; Newman, S.L.; Campagnoni, C.W.; Verdi, J.M.; Mohandas, T.; Handley, V.W.  
J. Neurochem. 54, 2032-2041, 1990  
A:Title: Expression of a novel transcript of the myelin basic protein gene.  
A:Reference number: A60920; MUID:90250449  
A:Accession: A60920  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 134-190;217-274;316-328 <KIT>  
A:Experimental source: M41; splice form 14K  
B:Grima, B.; Zelenika, D.; Pessac, B.  
J. Neurochem. 59, 2318-2323, 1992  
A:Title: A novel transcript overlapping the myelin basic protein gene.  
A:Reference number: I48407; MUID:93057537  
A:Accession: I48407  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-191,'SSEP' <GRI>  
A:Cross-references: EMBL:X67319; NID:g51332; PIDN:CAA47733.1; PID:g51333  
A:Note: submitted to the EMBL Data Library, July 1992  
R:Zeller, N.K.; Hunkeler, M.J.; Campagnoni, A.T.; Sprague, J.; Lazzarini, R.A.  
Proc. Natl. Acad. Sci. U.S.A. 81, 18-22, 1984  
A:Title: Characterization of mouse myelin basic protein messenger RNAs with a myelin bas  
A:Reference number: I58996; MUID:84119431  
A:Accession: I58996  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 219-248 <ZEL>  
A:Cross-references: GB:R00989; NID:g199037; PIDN:AAA39495.1; PID:g554195  
R:Miura, M.; Tanura, T.  
Gene 75, 31-38, 1989  
A:Title: The promoter elements of the mouse myelin basic protein gene function efficient  
A:Reference number: I54033; MUID:89252919  
A:Accession: I54033  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 134-157 <MIU>  
A:Cross-references: GB:M24410; NID:g199052; PIDN:AAA39498.1; PID:g554196  
R:Okano, H.; Tanura, T.; Miura, M.; Aoyama, A.; Ikenaka, K.; Oshimura, M.; Mikoshiba, K.  
EMBO J. 7, 77-83, 1988  
A:Title: Gene organization and transcription of duplicated MBP genes of myelin deficient  
A:Reference number: I53256; MUID:88196094  
A:Accession: I53256  
A>Status: translation not shown; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 217-229,'HN',232-250 <OKA>  
A:Cross-references: GB:M36275; NID:g199069; PIDN:AAA39504.1; PID:g293725  
A:Note: hypothetical translation of the reversed and complementary sequence to that show  
C:Comment: Mice have five forms of myelin basic protein: 21.5K, 18.5K, 17.24K, 17.22K and  
C:Genetics:  
A:Gene: Golli-mbp; shi-mld  
A:Introns: 190/3; 250/3; 262/3; 273/3; 314/3  
C:Function:  
A:Description: probably helps maintain myelin structure  
C:Superfamily: myelin basic protein  
C:Keywords: alternative splicing; myelin; structural protein  
F:1-190,217-276,316-328/Product: Golli-mbp protein (clone J37) #status predicted <MAL>  
F:134-328/Product: myelin basic protein, splice form 21.5K #status predicted <MAT>  
F:134-274,316-328/Product: myelin basic protein, splice form 17K-a #status predicted <MA  
F:134-190,217-328/Product: myelin basic protein, splice form 18.5K #status predicted <MA  
F:134-190,217-263,275-328/Product: myelin basic protein, splice form 17K-b #status predi  
F:134-190,217-274,316-328/Product: myelin basic protein, splice form 14K #status predict

Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 HYGSLPQKS-HGRTQDENP 18  
||||| ||||| ||||| ||||| |||||  
Db 224 HYGSLPQKSQHRTQDENP 242  
RESULT 3  
MBPGB  
myelin basic protein - chimpanzee (tentative sequence)  
N:Alternate names: MBP  
C:Species: Pan troglodytes (chimpanzee)  
C:Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 06-Sep-1996  
C:Accession: A03139  
R:Westall, F.C.; Thompson, M.; Kalter, S.S.  
Life Sci. 17, 219-223, 1975  
A:Title: The proposed sequence of the encephalitogenic protein from chimpanzee brain.  
A:Reference number: A03139; MUID:76009821  
A:Accession: A03139  
A:Molecule type: protein  
A:Residues: 1-171 <WES>  
C:Comment: This protein may function in maintaining the proper structure of myelin.  
C:Superfamily: myelin basic protein  
C:Keywords: blocked amino end; methylated amino acid; myelin; structural protein  
F:1/Modified site: blocked amino end (Ala) (probably acetylated) #status experimental  
F:107/Modified site: omega-N-methylarginine or omega-N,omega-N'-dimethylarginine (Arg

Query Match 82.5%; Score 85; DB 1; Length 171;  
Best Local Similarity 88.9%; Pred. No. 8.7e-07;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 HYGSLPQKSHGRTQDENP 18  
||||| ||||| ||||| ||||| |||||  
Db 68 HYGSLPQKSGHRTQDENP 85  
RESULT 4  
MBPGB  
myelin basic protein - pig (tentative sequence)  
N:Alternate names: myelin Al protein  
N:Contains: myelin basic protein amide 14  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 19-Apr-1996 #sequence\_revision 26-Apr-1996 #text\_change 07-May-1999  
C:Accession: A61640; A36245  
R:Kira, J.; Deibler, G.E.; Krutzsch, H.C.; Martenson, R.E.  
J. Neurochem. 44, 134-142, 1985  
A:Title: Amino acid sequence of porcine myelin basic protein.  
A:Reference number: A61640; MUID:85056964  
A:Accession: A61640  
A:Molecule type: protein  
A:Residues: 1-171 <KIR>  
A:Note: some peptides were ordered by homology  
R:Takamatsu, K.; Tatemoto, K.  
Biochem. Biophys. Res. Commun. 172, 1167-1174, 1990  
A:Title: Isolation and characterization of a novel peptide amide from porcine brain.  
A:Reference number: A36245; MUID:91058553  
A:Accession: A36245  
A:Molecule type: protein  
A:Residues: 1-14 <TAK>  
A:Note: the sequence in the abstract is inconsistent with that in figure 3 in having  
A:Note: this peptide has a carboxyl-terminal amide probably produced by a non-enzymat  
C:Superfamily: myelin basic protein  
C:Keywords: acetylated amino end; amidated carboxyl end; experimental autoimmune enc  
F:1-171/Product: myelin basic protein #status experimental <MAT>  
F:1-14/Product: myelin peptide amide-14 #status experimental <PAI2>  
F:1/Modified site: acetylated amino end (Ala) #status experimental  
F:14/Modified site: amidated carboxyl end (Tyr) (amide in mature form myelin peptide  
F:107/Modified site: omega-N-methylarginine or omega-N,omega-N'-dimethylarginine (Arg

Query Match 81.1%; Score 83.5; DB 1; Length 171;  
Best Local Similarity 84.2%; Pred. No. 1.6e-06;



A:Reference number: A94241; MUID:70178977  
 A:Contents: annotation  
 A:Note: the region including residues 114-122 induces experimental allergic encephalomyelitis in mice  
 C:Superfamily: myelin basic protein  
 C:Keywords: acetylated amino end; amidated carboxyl end; experimental autoimmune encephalomyelitis; myelin basic protein #status experimental <MAT>  
 F:1-169/Product: myelin basic protein #status experimental <MAT>  
 F:1-16/Product: myelin peptide amide-16 #status experimental <PA16>  
 F:1-12/Product: myelin peptide amide-12 #status experimental <PA12>  
 F:1-12/Product: myelin peptide amide-12 #status experimental <PA12>  
 F:1/Modified site: acetylated amino end (Ala) #status experimental  
 F:12/Modified site: amidated carboxyl end (Tyr) (amide in mature form myelin peptide amide)  
 F:16/Modified site: amidated carboxyl end (Ala) (amide in mature form myelin peptide amide)  
 F:106/Modified site: omega-N-methylarginine or omega-N'-dimethylarginine (Arg) (amide in mature form myelin peptide amide)  
 F:106/Modified site: omega-N-methylarginine or omega-N'-dimethylarginine (Arg) (amide in mature form myelin peptide amide)

Query Match 73.3%; Score 75.5; DB 1; Length 169;  
 Best Local Similarity 78.9%; Pred. No. 3.4e-05;  
 Matches 15; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 1 HYGSLPQKSHG-RTQDENP 18  
 ||||| |||||  
 Db 66 HYGSLPQKSHG-RTQDENP 84  
 ||||| |||||

RESULT 8  
 A37246  
 myelin basic protein - guinea pig  
 N:Alternate names: myelin A1 protein  
 C:Species: Cavia porcellus (guinea pig)  
 C:Date: 31-Jul-1991 #sequence\_revision 31-Jul-1991 #text\_change 07-Oct-1994  
 C:Accession: A37246; C92087; A03140  
 R:Deliber, G.E.; Martenson, R.E.; Krutzsch, H.C.; Kies, M.W.  
 J. Neurochem. 43, 100-105, 1984  
 A:Title: Sequence of guinea pig myelin basic protein.  
 A:Reference number: A37246; MUID:84215086  
 A:Accession: A37246  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-167 <DE>  
 R:Shapira, R.; McKeenly, S.S.; Chou, F.; Kibler, R.F.  
 J. Biol. Chem. 246, 4630-4640, 1971  
 A:Title: Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovine myelin basic protein.  
 A:Reference number: A92087  
 A:Accession: C92087  
 A:Molecule type: protein  
 A:Residues: 45-87 <SHA>  
 C:Superfamily: myelin basic protein  
 C:Keywords: myelin

Query Match 72.3%; Score 74.5; DB 2; Length 167;  
 Best Local Similarity 83.3%; Pred. No. 5e-05;  
 Matches 15; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 HYGSLPQKSHG-RTQDENP 18  
 ||||| |||||  
 Db 68 HYGSLPQKSHG-RTQDENP 84  
 ||||| |||||

RESULT 9  
 S08535  
 myelin basic protein - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 29-Jan-1993 #sequence\_revision 29-Jan-1993 #text\_change 13-Aug-1999  
 C:Accession: S08535  
 R:Zopf, D.; Sonntag, V.; Betz, H.; Gundelfinger, E.D.  
 Glia 2, 241-249, 1989  
 A:Title: Developmental accumulation and heterogeneity of myelin basic protein transcripts in the developing chick brain.  
 A:Reference number: S08535; MUID:89358239  
 A:Accession: S08535  
 A:Molecule type: mRNA  
 A:Residues: 1-174 <ZOP>  
 A:Cross-references: EMBL:X17103; NID:963594; PIDN:CAA34959.1; PID:963595  
 C:Superfamily: myelin basic protein

Query Match 61.7%; Score 63.5; DB 2; Length 174;  
 Best Local Similarity 63.2%; Pred. No. 0.0037;  
 Matches 12; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Qy 1 HYGSLPQKSHG-RTQDENP 18  
 ||||| |||||  
 Db 66 HYGSLPQKSHG-RTQDENP 84  
 ||||| |||||

RESULT 10  
 T35894  
 hypothetical protein SC9B10.25c - Streptomyces coelicolor  
 C:Species: Streptomyces coelicolor  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000  
 C:Accession: T35894  
 R:Olliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 submitted to the EMBL Data Library, November 1997  
 A:Reference number: Z21592  
 A:Accession: T35894  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-393 <OLI>  
 A:Cross-references: EMBL:AL009204; PIDN:CAA15815.1; GSPDB:GN00070; SCOEEDB:SC9B10.25c  
 A:Experimental source: strain A3(2)  
 C:Genetics:  
 C:Superfamily: tetracycline resistance protein

Query Match 46.6%; Score 48; DB 2; Length 393;  
 Best Local Similarity 50.0%; Pred. No. 3.8;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GSLPQKSHG-RTQDENP 18  
 ||||| |||||  
 Db 373 GTVEQTHGQDERP 389  
 ||||| |||||

RESULT 11  
 S41043  
 rum1 protein - fission yeast (Schizosaccharomyces pombe)  
 C:Species: Schizosaccharomyces pombe  
 C:Date: 31-Mar-1992 #sequence\_revision 14-Sep-1994 #text\_change 29-Oct-1999  
 C:Accession: S41043  
 R:Moreno, S.; Nurse, P.  
 Nature 367, 236-242, 1994  
 A:Title: Regulation of progression through the G1 phase of the cell cycle by the rum1 protein.  
 A:Reference number: S41043; MUID:94166876  
 A:Accession: S41043  
 A:Molecule type: DNA  
 A:Residues: 1-230 <MOR>  
 A:Cross-references: EMBL:X77730; NID:9456668; PIDN:CAA54786.1; PID:94566669  
 C:Genetics:  
 A:Gene: rum1  
 A:Map position: 2  
 C:Superfamily: Schizosaccharomyces rum1 protein

Query Match 44.7%; Score 46; DB 2; Length 230;  
 Best Local Similarity 64.3%; Pred. No. 4.5;  
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

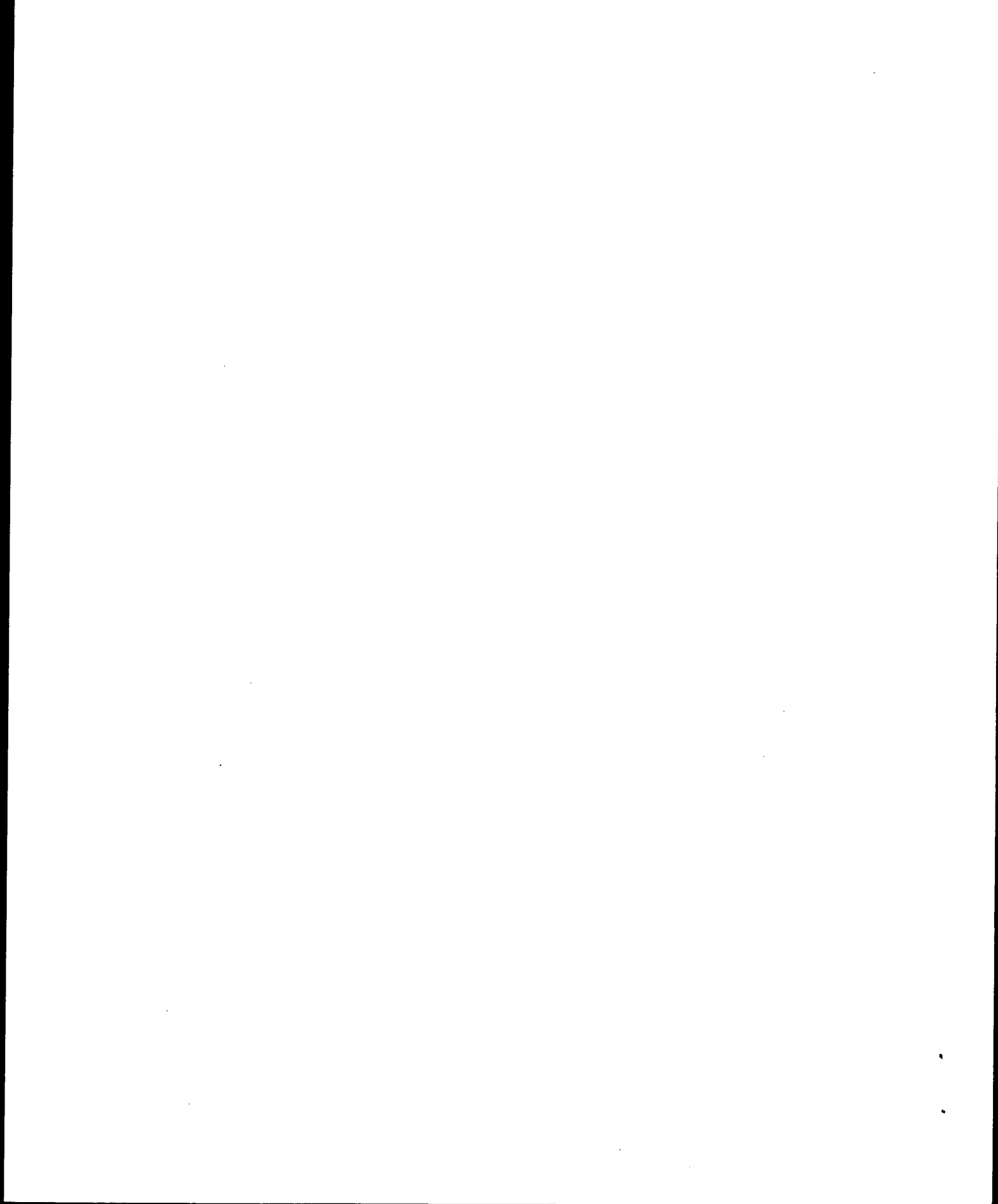
Qy 4 SLPLKSHG-RTQDENP 17  
 ||||| |||||  
 Db 211 SSFQKSRNTKDN 224  
 ||||| |||||

RESULT 12  
 T40233  
 Rum1p - fission yeast (Schizosaccharomyces pombe)  
 C:Species: Schizosaccharomyces pombe

A; Status: preliminary

Search completed:  
Job time: 177 sec







GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 28, 2002, 16:41:44 ; Search time 16.25 Seconds  
(without alignments)  
42.889 Million cell updates/sec

Title: US-09-813-383-1-copy\_8\_25  
Perfect score: 103  
Sequence: 1 HYGSLPKSHGRTQDENP 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	103	100.0	304	1 MBP_HUMAN	P02686 homo sapien
2	92.5	89.8	250	1 MBP_MOUSE	P04370 mus musculu
3	85	82.5	171	1 MBP_PANTR	P06906 pan troglod
4	83.5	81.1	171	1 MBP_PIG	P81558 sus scrofa
5	79	76.7	168	1 MBP_RABIT	P25274 oryctolagus
6	78.5	76.2	194	1 MBP_RAT	P02688 rattus norv
7	75.5	73.3	169	1 MBP_BOVIN	P02687 bos taurus
8	74.5	72.3	167	1 MBP_CAVPO	P25188 cavia porce
9	63.5	61.7	173	1 MBP_CHICK	P15720 gallus gall
10	46	44.7	230	1 RUM1_SCHPO	P40380 schizosacch
11	45	43.7	175	1 MBP_XENLA	P87346 xenopus lae
12	45	43.7	238	1 RNPH_HAENI	P44444 haemophilus
13	44	42.7	497	1 DHAL_EMENI	P08157 emericeila
14	43	41.7	497	1 DHAL_ASPNG	P41751 aspergillus
15	43	41.7	602	1 PEF2_LACLC	P94876 lactococcus
16	42	40.8	491	1 PM17_BOVIN	Q06154 bos taurus
17	42	40.8	546	1 PFH2_RAT	P07555 rattus norv
18	41	39.8	168	1 DRI1_MAIZE	P12950 zea mays (m
19	41	39.8	647	1 ZG48_XENLA	P18723 xenopus lae
20	41	39.8	932	1 YAI1A_SCHPO	Q09897 schizosacch
21	41	39.8	1180	1 EX5B_ECOLI	P08394 escherichia
22	40.5	39.3	676	1 RNR_CHLPN	Q92848 chlamydia p
23	40	38.8	187	1 RLNA_XENLA	P09897 xenopus lae
24	40	38.8	214	1 VIF_SIVSP	P19506 simian immu
25	40	38.8	477	1 MM11_XENLA	Q11005 xenopus lae
26	40	38.8	586	1 RRPO_BWYVF	P09507 beet wester
27	40	38.8	587	1 DHS4_COXBU	P31054 coxiella bu
28	39.5	38.3	506	1 30ID_RHOOP	Q04616 rhodococcus
29	39.5	38.3	850	1 D7_DICDI	P54692 dictyosteli
30	39	37.9	120	1 SODC_ASPJA	Q12548 aspergillus
31	39	37.9	151	1 SOD2_ORYSA	P28757 oryza sativ
32	39	37.9	214	1 VIF_SIVM1	P05903 simian immu
33	39	37.9	231	1 COR3_RABIT	Q28658 oryctolagus

34	39	37.9	333	1 ILVC_STRAW	Q59818 streptomyc
35	39	37.9	434	1 UL43_HSV11	P10227 herpes simp
36	39	37.9	655	1 ILFL_HUMAN	Q01167 homo sapien
37	39	37.9	660	1 AMY_BACSU	P00691 bacillus su
38	39	37.9	677	1 SGI_HUMAN	P05060 homo sapien
39	39	37.9	954	1 M3KA_HUMAN	Q02779 homo sapien
40	39	37.9	1136	1 POLG_OMV	P20234 o genome po
41	39	37.9	1227	1 PR16_HUMAN	Q92620 homo sapien
42	39	37.9	1256	1 FTNC_CHICK	P11722 gallus gall
43	39	37.9	1267	1 Y211_HUMAN	Q92610 homo sapien
44	38.5	37.4	151	1 SOD4_MAIZE	P23345 zea mays (m
45	38.5	37.4	151	1 SOD5_MAIZE	P23346 zea mays (m

## ALIGNMENTS

RESULT 1					
MBP_HUMAN					
ID	MBP_HUMAN	STANDARD;	PRT;	304 AA.	
AC	P02686; Q15337; Q15338; Q15339; Q15340;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	Myelin basic protein (MBP) (Myelin A1 protein) (Myelin membrane				
DE	encephalitogenic protein).				
GN	MBP.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).				
RC	TISSUE=Brain;				
RX	MEDLINE=94068468; PubMed=7504278;				
RA	Pribyl T.M., Campagnoni C.W., Kampf K., Kashima T., Handley V.W.,				
RA	McMahon J., Campagnoni A.T.;				
RT	"The human myelin basic protein gene is included within a 179-kilobase				
RT	transcription unit: expression in the immune and central nervous				
RT	systems."				
RL	Proc. Natl. Acad. Sci. U.S.A. 90:10695-10699(1993).				
RN	[2]				
RP	SEQUENCE FROM N.A. (ISOFORMS 3; 4; 5 AND 6).				
RC	TISSUE=Embryonic spinal cord;				
RX	MEDLINE=87311781; PubMed=2442403;				
RA	Roth H.J., Kronquist K.E., de Rosbo N., Crandall B.F.,				
RA	Campagnoni A.T.;				
RT	"Evidence for the expression of four myelin basic protein variants in				
RT	the developing human spinal cord through cDNA cloning."				
RL	J. Neurosci. Res. 17:321-328(1987).				
RN	[3]				
RP	SEQUENCE FROM N.A. (ISOFORM 6).				
RC	TISSUE=Embryonic spinal cord;				
RX	MEDLINE=86308101; PubMed=2427738;				
RA	Roth H.J., Kronquist K.E., Pretorius P.J., Crandall B.F.,				
RA	Campagnoni A.T.;				
RT	"Isolation and characterization of a cDNA coding for a novel human				
RT	17.3K myelin basic protein (MBP) variant."				
RL	J. Neurosci. Res. 16:227-238(1986).				
RN	[4]				
RP	SEQUENCE FROM N.A. (ISOFORMS 3 AND 5).				
RX	MEDLINE=86259714; PubMed=2425357;				
RA	Kamholz J., de Ferra F., Puckett C., Lazzarini R.A.;				
RA	"Identification of three forms of human myelin basic protein by cDNA				
RT	cloning."				
RL	Proc. Natl. Acad. Sci. U.S.A. 83:4962-4966(1986).				
RN	[5]				
RP	SEQUENCE FROM N.A. (ISOFORMS 3; 4; 5 AND 6).				
RX	MEDLINE=89302693; PubMed=2472816;				
RA	Streicher R., Stoffel W.;				
RA	"The organization of the human myelin basic protein gene. Comparison				
RT	with the mouse gene."				
RL	Biol. Chem. Hoppe-Seyler 370:503-510(1989).				



Query Match 100.0%; Score 103; DB 1; Length 304;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRQDENP 18  
 DB 202 HYGSLPQKSHGRQDENP 219

# RESULT 2 MBP\_MOUSE

ID MBP\_MOUSE STANDARD; PRT: 250 AA.  
 AC P04370; Q03139; Q01585; Q03176; Q9QWP1; Q99KE4; Q61837;  
 DT 20-MAR-1987 (Rel. 04, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Myelin basic protein (MBP) (Myelin A1 protein).  
 GN MBP OR SHI.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=93186801; PubMed=7680345;  
 RA Campagnoni A.T., Pribyl T.M., Campagnoni C.W., Kampf K.,  
 RA Anur-Umarjee S., Landry C.F., Handley V.W., Newman S., Garbay B.,  
 RA Kitamura K.;  
 RA "Structure and developmental regulation of Golli-mbp, a 105-kilobase  
 RT gene that encompasses the myelin basic protein gene and is expressed  
 RT in cells in the oligodendrocyte lineage in the brain.";  
 RL J. Biol. Chem. 268:4930-4938(1993).  
 RN [2]  
 RN SEQUENCE FROM N.A. (ISOFORM 2).  
 RC STRAIN=C57BL/6; TISSUE=Bone marrow;  
 RX MEDLINE=93057537; PubMed=1279125;  
 RA Grima B., Zelenika D., Pessac B.;  
 RA "A novel transcript overlapping the myelin basic protein gene.";  
 RT J. Neurochem. 59:2318-2323(1992).  
 RN [3]  
 RN SEQUENCE FROM N.A. (ISOFORMS 4; 5; 6 AND 8).  
 RX MEDLINE=86079555; PubMed=2416470;  
 RA de Ferra F., Eng H., Hudson L., Kamholz J., Puckett C., Molineaux S.,  
 RA Lazzarini R.A.;  
 RA "Alternative splicing accounts for the four forms of myelin basic  
 RT protein.";  
 RL Cell 43:721-727(1985).  
 RN [4]  
 RN SEQUENCE FROM N.A. (ISOFORM 5).  
 RX MEDLINE=85254913; PubMed=2410136;  
 RA Takahashi N., Roach A., Teplow D.B., Prusiner S.B., Hood L.E.;  
 RA "Cloning and characterization of the myelin basic protein gene from  
 RT mouse: one gene can encode both 14 kd and 18.5 kd MBPs by alternate  
 RT use of exons.";  
 RL Cell 42:139-148(1985).  
 RN [5]  
 RN SEQUENCE FROM N.A. (ISOFORM 6), AND SEQUENCE OF 9-194 FROM N.A.  
 RP (ISOFORM 7).  
 RC STRAIN=C57BL/6J; TISSUE=Brain;  
 RX MEDLINE=87118269; PubMed=2433693;  
 RA Newman S., Kitamura K., Campagnoni A.T.;  
 RA "Identification of a cDNA coding for a fifth form of myelin basic  
 RT protein in mouse.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:886-890(1987).  
 RN [6]  
 RN SEQUENCE FROM N.A. (ISOFORM 8).  
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King S., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [7]  
 RN SEQUENCE FROM N.A. (ISOFORM 9).  
 RP TISSUE=Breast tumor;  
 RA Strausberg R.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 RN [8]  
 RN SEQUENCE OF 135-157 FROM N.A.  
 RX MEDLINE=89252919; PubMed=2470651;  
 RA Miura M., Tamura T.A., Aoyama A., Mikoshiba K.;  
 RT "The promoter elements of the mouse myelin basic protein gene  
 RT function efficiently in NG108-15 neuronal/glia cells.";  
 RL Gene 75:31-38(1989).  
 RN [9]  
 RN PARTIAL SEQUENCE FROM N.A. (25 AA INSERTION OF ISOFORMS 4; 6 AND 9).  
 RP MEDLINE=86259714; PubMed=2425357;  
 RX Kamholz J., de Ferra F., Puckett C., Lazzarini R.A.;  
 RA "Identification of three forms of human myelin basic protein by cDNA  
 RT cloning.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:4962-4966(1986).  
 RN [10]  
 RN SEQUENCE OF 193-222 FROM N.A.  
 RX MEDLINE=84119431; PubMed=6198644;  
 RA Zeller N.K., Hunkeler M.J., Campagnoni A.T., Sprague J.,  
 RA Lazzarini R.A.;  
 RT "Characterization of mouse myelin basic protein messenger RNAs with a  
 RT myelin basic protein cDNA clone.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:18-22(1984).  
 RN [11]  
 RN PARTIAL SEQUENCE FROM N.A. (22 AA INSERTION OF ISOFORMS 10 AND 11).  
 RP TISSUE=Spinal cord;  
 RX MEDLINE=91162193; PubMed=1705957;  
 RA Aruga J., Okano H., Mikoshiba K.;  
 RT "Identification of the new isoforms of mouse myelin basic protein: the  
 RT existence of exon 5a.";  
 RL J. Neurochem. 56:1222-1226(1991).  
 RN [12]  
 RN PARTIAL SEQUENCE FROM N.A. (ISOFORMS 12; 13 AND 14).  
 RP MEDLINE=93203893; PubMed=7681106;  
 RX Nakajima K., Ikenaka K., Kagawa T., Aruga J., Nakao J., Nakahira K.,  
 RA Shiota C., Kim S.U., Mikoshiba K.;  
 RT "Novel isoforms of mouse myelin basic protein predominantly expressed  
 RT in embryonic stage.";  
 RL J. Neurochem. 60:1554-1563(1993).  
 RN [13]  
 RN SEQUENCE OF 191-224 FROM N.A.  
 RP MEDLINE=88196094; PubMed=2452084;  
 RX Okano H., Tamura T., Miura M., Aoyama A., Ikenaka K., Oshimura M.,  
 RA Mikoshiba K.;  
 RT "Gene organization and transcription of duplicated MBP genes of myelin  
 RT deficient (shi(mld)) mutant mouse.";  
 RL EMBO J. 7:77-83(1988).  
 RN [14]  
 RN DEVELOPMENTAL STAGE.  
 RP MEDLINE=98409779; PubMed=9736652;  
 RX Landry C.F., Pribyl T.M., Ellison J.A., Givogri M.I., Kampf K.,  
 RA Campagnoni C.W., Campagnoni A.T.;



Query Match 81.18; Score 83.5; DB 1; Length 171;  
 Best Local Similarity 84.28; Pred. No. 4.4e-07;  
 Matches 16; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGSLPQKSHGRQDENP 18  
 ||||| |||||  
 Db 68 HYGSLPQKSHGRQDENP 85

RESULT 4  
 MBP\_PIG STANDARD; PRT; 171 AA.  
 AC P81558; P98189;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Myelin basic protein (MBP).  
 GN MBP.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 [1]  
 RN SEQUENCE, AND METHYLATION OF ARG-107.  
 RP TISSUE=Brain;  
 RC MEDLINE=85056964; PubMed=2578056;  
 RA Kira J.-I., Deibler G.E., Krutzsch H.C., Martenson R.E.;  
 RT "Amino acid sequence of porcine myelin basic protein.";  
 RL J. Neurochem. 44:134-142(1985).  
 [2]  
 RN ERRATUM.  
 RA Kira J.-I., Deibler G.E., Krutzsch H.C., Martenson R.E.;  
 RL J. Neurochem. 44:1663-1663(1985).  
 CC -1- FUNCTION: Is, with PLP, the most abundant protein component of the  
 myelin membrane in the CNS. Has a role in both the formation and  
 stabilization of this compact multilayer arrangement of bilayers.  
 CC Each splice variant and charge isomer may have a specialized  
 function in the assembly of an optimized, biochemically functional  
 myelin membrane (By similarity).  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.  
 CC -1- PTM: As in other animals, several charge isomers may be produced  
 as a result of optional posttranslational modifications, such as  
 phosphorylation of serine or threonine residues, deamidation of  
 glutamine or asparagine residues, citrullination and methylation  
 of arginine residues.  
 CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.  
 DR HSSP; P02686; 1QCL.  
 DR InterPro: IPR000548; Myelin\_BP.  
 DR Pfam: PF01669; Myelin\_MBP; 1.  
 DR PRINTS; PR00212; MYELINMBP.  
 DR PROSITE; PS00569; MYELIN\_MBP; 1.  
 KW Myelin: Structural protein; Acetylation; Methylation; Phosphorylation;  
 Citrullination.  
 FT MOD\_RES 1 1 ACETYLATION.  
 FT MOD\_RES 7 7 PHOSPHORYLATION (PARTIAL) (BY  
 SIMILARITY).  
 FT MOD\_RES 25 25 CITRULLINATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 31 31 CITRULLINATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 55 55 PHOSPHORYLATION (PARTIAL) (BY  
 SIMILARITY).  
 FT MOD\_RES 98 98 PHOSPHORYLATION (PARTIAL) (BY  
 SIMILARITY).  
 FT MOD\_RES 103 103 DEAMIDATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 107 107 METHYLATION (MONO- OR DI-).  
 FT MOD\_RES 115 115 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 130 130 CITRULLINATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 148 148 DEAMIDATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 160 160 CITRULLINATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 162 162 PHOSPHORYLATION (PARTIAL) (BY  
 SIMILARITY).  
 FT MOD\_RES 166 166 PHOSPHORYLATION (PARTIAL) (BY  
 SIMILARITY).  
 FT MOD\_RES 171 171 CITRULLINATION (BY SIMILARITY).  
 SQ SEQUENCE 171 AA; 18487 MW; 287AEDF2F24028D9 CRC64;

Query Match 81.18; Score 83.5; DB 1; Length 171;  
 Best Local Similarity 84.28; Pred. No. 4.4e-07;  
 Matches 16; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGSLPQKSHGRQDENP 18  
 ||||| |||||  
 Db 67 HYGSLPQKSHGRQDENP 85

RESULT 5  
 MBP\_RABBIT STANDARD; PRT; 168 AA.  
 AC P25274;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Myelin basic protein (MBP) (Myelin P1 protein).  
 GN MBP.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 [1]  
 RN PRELIMINARY SEQUENCE.  
 RP TISSUE=Sciatic nerve;  
 RC MEDLINE=73190037; PubMed=4662101;  
 RA Brostoff S.W., Eylar E.H.;  
 RT "The proposed amino acid sequence of the P1 protein of rabbit sciatic  
 nerve myelin.";  
 RL Arch. Biochem. Biophys. 153:590-598(1972).  
 [2]  
 RN SEQUENCE OF 45-86.  
 RA Shapira R., McKenally S.S., Chou F., Kibler R.F.;  
 RT "Neurotrophic fragment of myelin basic protein. Amino acid  
 sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";  
 RL J. Biol. Chem. 246:4630-4640(1971).  
 [3]  
 RN PHOSPHORYLATION.  
 RA MEDLINE=83108902; PubMed=6185481;  
 RA Martenson R.E., Law M.J., Deibler G.E.;  
 RT "Identification of multiple in vivo phosphorylation sites in rabbit  
 myelin basic protein.";  
 RL J. Biol. Chem. 258:930-937(1983).  
 CC -1- FUNCTION: Is, with PLP, the most abundant protein component of the  
 myelin membrane in the CNS. Has a role in both the formation and  
 stabilization of this compact multilayer arrangement of bilayers.  
 CC Each splice variant and charge isomer may have a specialized  
 function in the assembly of an optimized, biochemically functional  
 myelin membrane (By similarity).  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.  
 CC -1- TISSUE SPECIFICITY: Found in both the central and the peripheral  
 nervous system.  
 CC -1- PTM: As in other animals, several charge isomers may be produced  
 as a result of optional posttranslational modifications, such as  
 phosphorylation of serine or threonine residues, deamidation of  
 glutamine or asparagine residues, citrullination and methylation  
 of arginine residues.  
 CC -1- PTM: The N-terminus is blocked.  
 CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.  
 DR PIR; B92087; B92087.  
 DR HSSP; P02686; 1QCL.  
 DR InterPro: IPR000548; Myelin\_BP.  
 DR PROSITE; PS00569; MYELIN\_MBP; PARTIAL.  
 KW Myelin: Structural protein; Acetylation; Methylation; Phosphorylation;  
 Citrullination; Autoimmune encephalomyelitis.  
 FT DOMAIN 45 86 INDUCES EXPERIMENTAL AUTOIMMUNE  
 ENCEPHALOMYELITIS (EAE).  
 FT MOD\_RES 1 1 ACETYLATION (PROBABLE).  
 FT MOD\_RES 7 7 PHOSPHORYLATION.  
 FT MOD\_RES 25 25 CITRULLINATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 31 31 CITRULLINATION (PARTIAL) (BY SIMILARITY).

FT MOD\_RES 56 56 PHOSPHORYLATION.  
 FT MOD\_RES 96 96 PHOSPHORYLATION.  
 FT MOD\_RES 101 101 DEAMIDATION (PARTIAL) (PROBABLE).  
 FT MOD\_RES 105 105 METHYLATION (MONO- OR DI-).  
 FT MOD\_RES 113 113 PHOSPHORYLATION.  
 FT MOD\_RES 128 128 CITRULLINATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 145 145 DEAMIDATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 157 157 CITRULLINATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 159 159 PHOSPHORYLATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 163 163 PHOSPHORYLATION.  
 FT MOD\_RES 168 168 CITRULLINATION (BY SIMILARITY).  
 FT CONFLICT 46 46 S -> G (IN REF. 2).  
 SQ SEQUENCE 168 AA; 18217 MW; EC3C97ACD2C08EA6 CRC64;

Query Match 76.7%; Score 79; DB 1; Length 168;  
 Best Local Similarity 83.3%; Pred. No. 2.5e-06;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 HYGSLPQKSHGRDQENP 18

Db 66 HYGSLPQKSHGRDQENP 83

## RESULT 6

MBP\_RAT ID MBP\_RAT STANDARD; PRT; 194 AA.  
 AC P02688; Q9Z1J4; Q9Z1J5; Q9Z1J6;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Myelin basic protein S (MBP S).  
 GN MBP.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).  
 RA Lobell A.M., Wigzell H.;  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 4).  
 RX MEDLINE=87026249; PubMed=2429678;  
 RA Schleich M., Budzinski R.M., Stoffel W.;  
 RT "Cloned proteolipid protein and myelin basic protein cDNA.  
 Transcription of the two genes during myelination.";  
 RL Biol. Chem. Hoppe-Seyler 367:825-834(1986).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 4).  
 RX MEDLINE=84026484; PubMed=6194889;  
 RA Roach A., Boylan K.B., Horvath S., Prusiner S.B., Hood L.E.;  
 RT "Characterization of cloned cDNA representing rat myelin basic  
 protein: absence of expression in brain of shiverer mutant mice.";  
 RL Cell 34:799-806(1983).  
 RN [4]  
 RP SEQUENCE (ISOFORM 4).  
 RX MEDLINE=75127359; PubMed=4141893;  
 RA Dunkley P.R., Carnegie P.R.;  
 RT "Amino acid sequence of the smaller basic protein from rat brain  
 myelin.";  
 RL Biochem. J. 141:243-255(1974).  
 RN [5]  
 RP SEQUENCE OF 130-194 FROM N.A.  
 RX STRAIN=Lewis; TISSUE=Brain;  
 RC MEDLINE=96078224; PubMed=7578863;  
 RA Malotka J., Doramair K.;  
 RT "Alternative splicing and cDNA sequence of myelin basic protein gene  
 of the Lewis rat.";  
 RL Autoimmunity 20:67-68(1995).  
 RN [6]  
 RP SEQUENCE OF 45-111 (ISOFORM 4).

RX MEDLINE=73180720; PubMed=4123234;  
 RA McFarlin D.E., Blank S.E., Kibler R.F., McKneally S.S., Shapiro R.;  
 RT "Experimental allergic encephalomyelitis in the rat: response to  
 encephalitogenic proteins and peptides.";  
 RL Science 179:478-480(1973).  
 CC -!- FUNCTION: Is, with PLP, the most abundant protein component of the  
 myelin membrane in the CNS. Has a role in both the formation and  
 stabilization of this compact multilayer arrangement of bilayers.  
 CC Each splice variant and charge isomer may have a specialized  
 function in the assembly of an optimized, biochemically functional  
 myelin membrane (By similarity).  
 CC -!- SUBUNIT: Homodimer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.  
 CC -!- ALTERNATIVE PRODUCTS: At least 4 isoforms; 1/21.5 kDa (shown  
 here), 2/18.5 kDa, 3/17 kDa and 4/14 kDa; are produced by  
 alternative splicing.  
 CC -!- TISSUE SPECIFICITY: Found in both the central and the peripheral  
 nervous system.  
 CC -!- PTM: As in other animals, several charge isomers may be produced  
 as a result of optional posttranslational modifications, such as  
 phosphorylation of serine or threonine residues, deamidation of  
 glutamine or asparagine residues, citrullination and methylation  
 of arginine residues.  
 CC -!- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.  
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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC EMBL; AJ132895; CAA10804.1; -;  
 CC EMBL; AJ132896; CAA10805.1; -;  
 CC EMBL; AJ132897; CAA10806.1; -;  
 CC EMBL; AJ132898; CAA10807.1; -;  
 CC EMBL; M25889; AAA41575.1; -;  
 CC EMBL; K00512; -; NOT\_ANNOTATED\_CDS.  
 CC EMBL; X72392; -; NOT\_ANNOTATED\_CDS.  
 CC PIR; A03142; MERTS.  
 CC PIR; B24351; B24351.  
 CC PIR; A21062; A21062.  
 CC HSSP; P02686; LOCL.  
 CC InterPro: IPR000548; Myelin\_BP.  
 CC Pfam: PF01669; Myelin\_MBP; 1.  
 CC PRINTS; PR00212; MYELINMBP.  
 CC PROSITE; PS00569; MYELIN\_MBP; 1.  
 KW Myelin; Structural protein; Acetylation; Methylation; Phosphorylation;  
 KW Citrullination; Autoimmune encephalomyelitis; Alternative splicing.  
 FT INIT\_MET 0 0  
 FT MOD\_RES 1 1 ACETYLATION.  
 FT MOD\_RES 7 7 PHOSPHORYLATION (PARTIAL) (BY  
 SIMILARITY).  
 FT MOD\_RES 25 25 CITRULLINATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 31 31 CITRULLINATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 56 56 PHOSPHORYLATION (PARTIAL) (BY  
 SIMILARITY).  
 FT MOD\_RES 121 121 PHOSPHORYLATION (PARTIAL) (BY  
 SIMILARITY).  
 FT MOD\_RES 126 126 DEAMIDATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 130 130 METHYLATION (MONO- OR DI-).  
 FT MOD\_RES 138 138 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 153 153 CITRULLINATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 171 171 DEAMIDATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 183 183 CITRULLINATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 185 185 PHOSPHORYLATION (PARTIAL) (BY  
 SIMILARITY).  
 FT MOD\_RES 189 189 PHOSPHORYLATION (PARTIAL) (BY  
 SIMILARITY).  
 FT MOD\_RES 194 194 CITRULLINATION (BY SIMILARITY).  
 FT MOD\_RES 59 84 MISSING (IN ISOFORM 2 AND ISOFORM 4).  
 FT VARSPLIC 140 180 MISSING (IN ISOFORM 3 AND ISOFORM 4).

FT CONFLICT 46 47 SG -> GS (IN REF. 6).  
 FT CONFLICT 191 191 M -> I (IN REF. 1 AND 3).  
 SQ SEQUENCE 194 AA; 21371 MW; 68FB399C250B4C50 CRC64;

Query Match 76.2%; Score 78.5; DB 1; Length 194;  
 Best Local Similarity 88.9%; Pred. No. 3.6e-06;  
 Matches 16; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 HYGSLPQKSHGRTOENP 18  
 ||||||| |||||  
 Db 92 HYGSLPQKSO-RTQDENP 108

RESULT 7  
 MBP\_BOVIN STANDARD; PRT; 169 AA.  
 AC P02687; Q9TSA6; Q9TSG3; Q9BGW6;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Myelin basic protein (MBP) (Myelin A1 protein) (20 kDa microtubule  
 stabilizing protein).  
 GN MBP.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=72007306; PubMed=5096093;  
 RA Eylar E.H., Brostoff S.W., Hashim G., Caccam J., Burnett P.;  
 RT "Basic A1 protein of the myelin membrane. The complete amino acid  
 sequence.";  
 RL J. Biol. Chem. 246:5770-5784(1971).  
 RN [2]  
 RP REVISION.  
 RX MEDLINE=74070688; PubMed=4129204;  
 RA Brostoff S.W., Reuter W., Hichens M., Eylar E.H.;  
 RT "Specific cleavage of the A1 protein from myelin with cathepsin D.";  
 RL J. Biol. Chem. 249:559-567(1974).  
 RN [3]  
 RP SEQUENCE OF 4-56 FROM N.A.  
 RA Pietrowski D., Medugorac I., Foerster M.;  
 RT "A new MBP allele in Bos taurus is characterized by BseNI PCR-RFLP.";  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 43-87.  
 RA Shapira R., McNeally S.S., Chou F.C.-H., Kibler R.F.;  
 RT "Encephalitogenic fragment of myelin basic protein. Amino acid  
 sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";  
 RL J. Biol. Chem. 246:4630-4640(1971).  
 RN [5]  
 RP SEQUENCE OF 38-58 AND 119-141.  
 RC TISSUE=Brain;  
 RX MEDLINE=93003019; PubMed=1382581;  
 RA Pirolet F., Derancourt J., Halech J., Job D., Margolis R.L.;  
 RT "Ca(2+)-calmodulin regulated effectors of microtubule stability in  
 bovine brain.";  
 RL Biochemistry 31:8849-8855(1992).  
 RN [6]  
 RP SEQUENCE OF 30-42; 74-89 AND 114-129.  
 RX MEDLINE=96107211; PubMed=8530487;  
 RA Prasad K., Barouch W., Martin B.M., Greene L.E., Eisenberg E.;  
 RT "Purification of a new clathrin assembly protein from bovine brain  
 coated vesicles and its identification as myelin basic protein.";  
 RL J. Biol. Chem. 270:30551-30556(1995).  
 RN [7]  
 RP SYNTHESIS OF ALLERGIC ENCEPHALOMYELITIS INDUCING REGION.  
 RX MEDLINE=70178977; PubMed=5442707;  
 RA Eylar E.H., Caccam J., Jackson J.J., Westall F.C., Robinson A.B.;  
 RT "Experimental allergic encephalomyelitis: synthesis of

RT disease-inducing site of the basic protein.";  
 RL Science 168:1220-1223(1970).  
 RN [8]  
 RP METHYLATION.  
 RX MEDLINE=71153946; PubMed=4994464;  
 RA Brostoff S.W., Eylar E.H.;  
 RT "Localization of methylated arginine in the A1 protein from myelin.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 68:765-769(1971).  
 RN [9]  
 RP POST-TRANSLATIONAL MODIFICATIONS.  
 RX MEDLINE=76167591; PubMed=57115;  
 RA Chou F.C.-H., Chou C.-H.J., Shapira R., Kibler R.F.;  
 RT "Basis of microheterogeneity of myelin basic protein.";  
 RL J. Biol. Chem. 251:2671-2679(1976).  
 RN [10]  
 RP SEQUENCE OF 97-104, AND PHOSPHORYLATION OF THR-97.  
 RX MEDLINE=91060584; PubMed=1700979;  
 RA Erickson A.K., Payne D.M., Martino P.A., Rossomando A.J.,  
 RA Shabanowitz J., Weber M.J., Hunt D.F., Sturgill T.W.;  
 RT "Identification by mass spectrometry of threonine 97 in bovine myelin  
 basic protein as a specific phosphorylation site for mitogen-activated  
 protein kinase.";  
 RL J. Biol. Chem. 265:19728-19735(1990).  
 RN [11]  
 RP POST-TRANSLATIONAL MODIFICATIONS.  
 RX MEDLINE=98153125; PubMed=9485392;  
 RA Zand R., Li M.X., Jin X., Lubman D.;  
 RT "Determination of the sites of posttranslational modifications in the  
 charge isomers of bovine myelin basic protein by capillary  
 electrophoresis-mass spectroscopy.";  
 RL Biochemistry 37:2441-2449(1998).  
 RN [12]  
 RP DIMERIZATION.  
 RX MEDLINE=80198320; PubMed=6155143;  
 RA Smith R.;  
 RT "Sedimentation analysis of the self-association of bovine myelin basic  
 protein.";  
 RL Biochemistry 19:1826-1831(1980).  
 CC -1- FUNCTION: Is, with PLP, the most abundant protein component of the  
 myelin membrane in the CNS. Has a role in both the formation and  
 stabilization of this compact multilayer arrangement of bilayers.  
 CC Each splice variant and charge isomer may have a specialized  
 function in the assembly of an optimized, biochemically functional  
 myelin membrane (By similarity).  
 CC -1- SUBUNIT: Homodimer; self-associates in the presence of lysolipid.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.  
 CC -1- TISSUE SPECIFICITY: Found in both the central and the peripheral  
 nervous system.  
 CC -1- PTM: At least 6 charge isomers; C1 (the most cationic and least  
 modified form), C2, C3, C4, C5 AND C6 (the less cationic form);  
 CC are produced as a result of optional posttranslational  
 CC modifications, such as phosphorylation of serine or threonine  
 CC residues, deamidation of glutamine or asparagine residues,  
 CC citrullination and methylation of arginine residues.  
 CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.  
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 CC -----  
 CC EMBL; AF226693; AAK00645.1;  
 CC PIR; A03140; MBBOB.  
 CC HSP; P02686; 1OCL.  
 CC InterPro: IPR000548; Myelin\_BP.  
 CC Pfam: PF01669; Myelin\_MBP.1.  
 CC PRINTS; PR00212; MYELINMBP.  
 CC PROSITE; PS00569; MYELIN\_MBP; 1.  
 CC Myelin: Structural protein; Acetylation; Methylation; Phosphorylation;  
 CC Citrullination; Autoimmune encephalomyelitis.  
 KW

FT DOMAIN 43 87 INDUCES EXPERIMENTAL AUTOIMMUNE  
 FT DOMAIN 114 122 INDUCES EXPERIMENTAL AUTOIMMUNE  
 FT MOD\_RES 1 1 ACETYLLATION.  
 FT MOD\_RES 7 7 PHOSPHORYLATION (IN C5 AND C6).  
 FT MOD\_RES 23 23 CITRULLINATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 29 29 CITRULLINATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 54 54 PHOSPHORYLATION (IN C4, C5 AND C6).  
 FT MOD\_RES 97 97 PHOSPHORYLATION (BY MAPK) (IN C3, C4, C5 AND C6).  
 FT MOD\_RES 102 102 DEAMIDATION (IN C5).  
 FT MOD\_RES 106 106 METHYLATION (MONO- OR DI-).  
 FT MOD\_RES 114 114 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 129 129 CITRULLINATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 146 146 DEAMIDATION (IN C2).  
 FT MOD\_RES 158 158 CITRULLINATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 160 160 PHOSPHORYLATION (IN C4 AND C6).  
 FT MOD\_RES 164 164 PHOSPHORYLATION (IN C3, C5 AND C6).  
 FT MOD\_RES 169 169 CITRULLINATION (PROBABLE).  
 SQ SEQUENCE 169 AA; 18323 MW; 8E1157B7A1978484 CRC64;

Query Match 73.3%; Score 75.5; DB 1; Length 169;  
 Best Local Similarity 78.9%; Pred. No. 1e-05;

Matches 15; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 1 HYGSLPQKSHG-RTQDENP 18  
 |||||: |||||  
 Db 66 HYGSLPQKSHG-RTQDENP 84

## RESULT 8

ID MBP\_CAVPO STANDARD; PRT; 167 AA.  
 AC P25188;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Myelin basic protein (MBP).  
 GN MBP.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE=84215086; PubMed=6202840;  
 RA Deibler G.E., Martenson R.E., Krutzsch H.C., Kies M.W.;  
 RT "Sequence of guinea pig myelin basic protein.";  
 RL J. Neurochem. 43:100-105(1984).  
 RN [2]  
 RP SEQUENCE OF 7-156 FROM N.A.  
 RC STRAIN=Hartley; TISSUE=Spinal cord;  
 RA Kim G., Tanuma N., Matsumoto Y.;  
 RT "DNA vaccination using Guinea pig myelin basic protein coding region  
 in experimental autoimmune encephalomyelitis.";  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 45-87.  
 RA Shapira R., McNeally S.S., Chou F., Kibler R.F.;  
 RT "Encephalitogenic fragment of myelin basic protein. Amino acid  
 sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";  
 RL J. Biol. Chem. 246:4630-4640(1971).  
 RN [4]  
 RP POST-TRANSLATIONAL MODIFICATIONS.  
 RX MEDLINE=76025020; PubMed=51849;  
 RA Deibler G.E., Martenson R.E., Kramer A.J., Kies M.W.;  
 RT "The contribution of phosphorylation and loss of COOH-terminal  
 arginine to the microheterogeneity of myelin basic protein.";  
 RL J. Biol. Chem. 250:7931-7938(1975).  
 CC -!- FUNCTION: Is, with PLP, the most abundant protein component of the  
 myelin membrane in the CNS. Has a role in both the formation and

CC stabilization of this compact multilayer arrangement of bilayers.  
 CC Each splice variant and charge isomer may have a specialized  
 CC function in the assembly of an optimized, biochemically functional  
 CC myelin membrane (By similarity).  
 CC -!- SUBUNIT: Homodimer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.  
 CC -!- TISSUE SPECIFICITY: Found in both the central and the peripheral  
 CC nervous system.  
 CC -!- PTM: At least 5 charge isomers: C1 (the most cationic, least  
 CC modified, and most abundant form), C2, C3, C4 and C5 (the less  
 CC cationic form); are produced as a result of optional  
 CC posttranslational modifications such as phosphorylation of serine  
 CC or threonine residues, deamidation of glutamine or asparagine  
 CC residues, citrullination and methylation of arginine residues. C1  
 CC and C2 are unphosphorylated, C3 and C4 are monophosphorylated and  
 CC C5 is phosphorylated at two positions.  
 CC -!- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.  
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 CC EMBL; AF074337; AAC26130.1; -;  
 DR PIR; A37246; A37246.  
 DR PIR; C92087; C92087.  
 DR HSP; P02686; IQCL.  
 DR InterPro; IPR000548; Myelin\_BP.  
 DR Pfam; PF01669; Myelin\_MBP; 1.  
 DR PRINTS; PR00212; MYELINMBP.  
 DR PROSITE; PS00569; MYELIN\_MBP; 1.  
 KW Myelin; Structural protein; Acetylation; Methylation; Phosphorylation;  
 KW Citrullination; Autoimmune encephalomyelitis;  
 FT DOMAIN 45 87 INDUCES EXPERIMENTAL AUTOIMMUNE  
 FT DOMAIN 114 122 INDUCES EXPERIMENTAL AUTOIMMUNE  
 FT MOD\_RES 1 1 ACETYLLATION.  
 FT MOD\_RES 7 7 PHOSPHORYLATION (PARTIAL) (BY  
 FT SIMILARITY).  
 FT MOD\_RES 25 25 CITRULLINATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 31 31 CITRULLINATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 56 56 PHOSPHORYLATION (PARTIAL) (BY  
 FT SIMILARITY).  
 FT MOD\_RES 97 97 PHOSPHORYLATION (PARTIAL) (BY  
 FT SIMILARITY).  
 FT MOD\_RES 102 102 DEAMIDATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 106 106 METHYLATION (MONO-OR DI-) (BY  
 FT SIMILARITY).  
 FT MOD\_RES 114 114 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 129 129 CITRULLINATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 144 144 DEAMIDATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 156 156 CITRULLINATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 158 158 PHOSPHORYLATION (PARTIAL) (BY  
 FT SIMILARITY).  
 FT MOD\_RES 162 162 PHOSPHORYLATION (PARTIAL) (BY  
 FT SIMILARITY).  
 FT MOD\_RES 167 167 CITRULLINATION (BY SIMILARITY).  
 SQ SEQUENCE 167 AA; 18213 MW; 866D31F1E5ACFEA6 CRC64;

Query Match

Best Local Similarity 72.3%; Score 74.5; DB 1; Length 167;

Matches 15; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 HYGSLPQKSHGRTQDENP 18  
 |||||: |||||  
 Db 68 HYGSLPQKSHGRTQDENP 84



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RESULT 9
MBP_CHICK
ID MBP_CHICK STANDARD; PRT: 173 AA.
AC P15720;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Myelin basic protein (MBP).
GN MBP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX STRAIN=White Leghorn; TISSUE=Optic lobe;
RA MEDLINE=89338239; PubMed=2475444;
RA Zopf D., Sonntag H., Betz H., Gundelfinger E.D.;
RT "Developmental accumulation and heterogeneity of myelin basic protein
transcripts in the chick visual system.";
RL Glia 2:241-249(1989).
CC -!- FUNCTION: Is, with PLP, the most abundant protein component of the
myelin membrane in the CNS. Has a role in both the formation and
stabilization of this compact multilayer arrangement of bilayers.
CC Each splice variant and charge isomer may have a specialized
function in the assembly of an optimized, biochemically functional
myelin membrane (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
CC -!- ALTERNATIVE PRODUCTS: At least 2 isoforms; 1 (major form) (shown
here) and 2; are produced by alternative splicing.
CC -!- DEVELOPMENTAL STAGE: In the optic lobe, first detected at
embryonic day 14. Expression strongly increases between embryonic
days 16 and 18, reaches a maximum at postnatal day 1, and then
declines again to the adult level.
CC -!- PTM: As in other animals, several charge isomers may be produced
as a result of optional posttranslational modifications, such as
phosphorylation of serine or threonine residues, deamidation of
glutamine or asparagine residues, citrullination and methylation
of arginine residues.
CC -!- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
CC
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CC
CC EMBL; X17103; CAA34959.1; -.
CC PIR; S08535; S08535.
CC HSSP; P02686; 1QCU.
CC InterPro; IPR000548; Myelin_Bp.
CC Pfam; PF01669; Myelin_MBP; 1.
CC PRINTS; PR00212; MYELINMBP.
CC PROSITE; PS00569; MYELIN_MBP; 1.
KW Myelin; Structural protein; Acetylation; Methylation; Phosphorylation;
KW Citrullination; Alternative splicing.
FT INIT_MET 0 0 BY SIMILARITY.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT MOD_RES 7 7 PHOSPHORYLATION (PARTIAL) (BY
SIMILARITY).
FT MOD_RES 24 24 CITRULLINATION (PARTIAL) (BY SIMILARITY).
FT MOD_RES 29 29 CITRULLINATION (PARTIAL) (BY SIMILARITY).
FT MOD_RES 96 96 PHOSPHORYLATION (PARTIAL) (BY
SIMILARITY).
FT MOD_RES 101 101 DEAMIDATION (PARTIAL) (BY SIMILARITY).
FT MOD_RES 105 105 METHYLATION (MONO-OR DI-) (BY
SIMILARITY).
FT MOD_RES 113 113 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 146 146 DEAMIDATION (PARTIAL) (BY SIMILARITY).
FT

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FT MOD_RES 164 164 PHOSPHORYLATION (PARTIAL) (BY
SIMILARITY).
FT MOD_RES 168 168 PHOSPHORYLATION (PARTIAL) (BY
SIMILARITY).
FT MOD_RES 173 173 CITRULLINATION (BY SIMILARITY).
FT VARSPLIC 104 114 MISSING (IN ISOFORM 2).
SQ SEQUENCE 173 AA; 18677 MW; ABFE70D4C9CF019D CRC64;

Query Match 61.7%; Score 63.5; DB 1; Length 173;
Best Local Similarity 63.3%; Pred. No. 0.0011;
Matches 12; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 HYGSLPQKS-HGRTQDENP 18
| | | | | | | | | | | | | |
DB 65 HVGSIQRQSHGRCDDNP 83
| | | | | | | | | | | | | |

RESULT 10
RUM1_SCHPO
ID RUM1_SCHPO STANDARD; PRT: 230 AA.
AC P40380; O74373;
DT 01-FEB-1995 (Rel. 31, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein rum1 (p25-rum1).
GN RUM1 OR SPBC32F12.09.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=94166876; PubMed=8121488;
RA Moreno S., Nurse P.;
RT "Regulation of progression through the G1 phase of the cell cycle by
the rum1+ gene.";
RN Nature 367:236-242(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Moreno S., Wood V., Rajandream M.A., Barrell B.G.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: REGULATOR OF CELL CYCLE G1 PHASE PROGRESSION. PROBABLY
INTERACTS WITH CDC2 TO INHIBITS ITS ACTION UNTIL THE CELL MASS FOR
START IS REACHED.
CC
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CC
CC EMBL; X77730; CAA54786.1; -.
CC PIR; S41043; S41043.
KW Cell cycle.
FT CONFLICT 72 73 ML -> IV (IN REF. 1).
SQ SEQUENCE 230 AA; 25288 MW; C5199FE345F7484A CRC64;

Query Match 44.7%; Score 46; DB 1; Length 230;
Best Local Similarity 64.3%; Pred. No. 1.5;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 SLPOKSHGRTQDEN 17
| | | | | | | | | |
DB 211 SSPQKSRSNKDEN 224
| | | | | | | | | |

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Query Match      43.7%; Score 45; DB 1; Length 238;
Best Local Similarity 53.3%;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      2 YGSLPQKSHGRTQDE 16
      |||::|||
Db      63 YGMLPSTHSRMORE 77

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RESULT 13
DHAL_EMENI STANDARD; PRT: 497 AA.
AC P08157;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Aldehyde dehydrogenase (EC 1.2.1.3) (ALDDH).
GN ALDA OR ASPA.
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=5072;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=8724800; PubMed=3036652;
RX Pickett M., Gwynne D.I., Buxton F.P., Elliott R., Davies R.W.,
RA Lockington R.A., Scazzocchio C., Sealy-Lewis H.M.;
RT "Cloning and characterization of the alda gene of Aspergillus
RT nidulans."
RL Gene 51:217-226(1987).
CC -1- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH.
CC -1- PATHWAY: SECOND STEP IN ETHANOL UTILIZATION.
CC -1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
CC
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CC
CC EMBL: M16197; AAA3293.1; -.
DR HSP; P05091; ICW3.
DR InterPro: IPR002086; Aldehyde_dehydr.
PFam: PF00171; aldedh; 1.
DR PROSITE: PS00070; ALDEHYDE_DEHYDR_CYS; 1.
DR PROSITE: PS00687; ALDEHYDE_DEHYDR_GLU; 1.
KW Oxidoreductase; NAD.
FT NP_BIND 241 246 NAD (ADP PART) (BY SIMILARITY).
FT ACT_SITE 264 264 BY SIMILARITY.
FT ACT_SITE 298 298 BY SIMILARITY.
SQ SEQUENCE 497 AA; 54088 MW; 1711FCEA993E571B CRC64;

Query Match 42.7%; Score 44; DB 1; Length 497;
Best Local Similarity 44.4%; Pred. No. 7 8;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
: | | | | | | |
Db 127 YYAGWADKINGQTIDNP 144

RESULT 14
DHAL_ASPNG STANDARD; PRT: 497 AA.
AC P41751;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Aldehyde dehydrogenase (EC 1.2.1.3) (ALDDH).
GN ALDA.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=90108706; PubMed=2606357;
RX O'Connell M.J., Kelly J.M.;
RT "Physical characterization of the aldehyde-dehydrogenase-encoding
RT gene of Aspergillus niger."
RL Gene 84:173-180(1989).
CC -1- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH.
CC -1- PATHWAY: SECOND STEP IN ETHANOL UTILIZATION.
CC -1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
CC
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CC
CC EMBL: M32351; AAA87596.1; -.
DR HSP; P05091; ICW3.
DR InterPro: IPR002086; Aldehyde_dehydr.
PFam: PF00171; aldedh; 1.
DR PROSITE: PS00070; ALDEHYDE_DEHYDR_CYS; 1.
DR PROSITE: PS00687; ALDEHYDE_DEHYDR_GLU; 1.
KW Oxidoreductase; NAD.
FT NP_BIND 242 247 NAD (ADP PART) (BY SIMILARITY).
FT ACT_SITE 265 265 BY SIMILARITY.
FT ACT_SITE 299 299 BY SIMILARITY.
SQ SEQUENCE 497 AA; 53809 MW; 47CA353FFD8A50E8 CRC64;

Query Match 41.7%; Score 43; DB 1; Length 497;
Best Local Similarity 47.1%; Pred. No. 12;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDEN 17
: | | | | | | |
Db 128 YYGWADKINGQTIDTN 144

RESULT 15
PEF2_LACLC STANDARD; PRT: 602 AA.
ID PEF2_LACLC
AC P94876;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Oligoendopeptidase F, chromosomal (EC 3.4.24.-).
GN PEPF2.
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Lactococcus.
OX NCBI_TaxID=1359;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=NCDO 763;
RX MEDLINE=97352670; PubMed=9209029;
RA Nardi M., Renault P., Monnet V.;
RT "Duplication of the pepF gene and shuffling of DNA fragments on the
RT lactose plasmid of Lactococcus lactis."
RL J. Bacteriol. 179:4164-4171(1997).
CC -1- FUNCTION: HYDROLYZES PEPTIDES CONTAINING BETWEEN 7 AND 17 AMINO
CC ACIDS WITH A RATHER WIDE SPECIFICITY.
CC -1- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3.
CC
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CC

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DR EMBL: X99710; CAA68044.1; -.  
 DR InterPro: IPR001567; Peptidase\_M3.  
 DR InterPro: IPR000130; Zn\_Mpeptidse.  
 DR Pfam: PF01432; Peptidase\_M3; 1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; 1.  
 KW Hydrolase; Metalloprotease; Zinc.  
 FT METAL 388 388 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT ACT\_SITE 389 389 BY SIMILARITY.  
 FT METAL 392 392 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT METAL 395 395 ZINC (CATALYTIC) (BY SIMILARITY).  
 SQ SEQUENCE 602 AA; 69990 MW; D02235F1748BIADF CRC64;

Query Match 41.7%; Score 43; DB 1; Length 602;  
 Best Local Similarity 47.1%; Pred. NO. 14;  
 Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 2 YGSLPKSHGHRTQDENP 18  
 ||| : : : : |||  
 Db 487 YGELNEKYGYLSAKENP 503

Search completed: August 28, 2002, 16:41:45  
 Job time: 372 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 28, 2002, 16:41:23 ; Search time 41.39 Seconds  
(without alignments)  
75.233 Million cell updates/sec

Title: US-09-813-383-1\_COPY\_8\_25  
Perfect score: 103  
Sequence: 1 HYGSLPQKSHGRTQDENP 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters:

```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

```

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Database :
SPREMBL_19:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.potent:*
12: sp.virus:*
13: sp.invertebrate:*
14: sp.unclassified:*
15: sp.rvirus:*
16: sp.bacteriap:*
17: sp.archaeap:*
```

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	%		Length	DB	ID	Description
		Match					
1	50	48.5	238	2	Q9AES0	Q9aes0	pasteurella
2	48	46.6	393	2	O50532	O50532	streptomyce
3	47.5	46.1	1123	10	Q9LH08	Q9lh08	arabidopsis
4	47	45.6	235	2	Q9XS28	Q9xs28	legionella
5	46	44.7	257	16	Q9KV06	Q9kv06	vibrio chol
6	46	44.7	632	16	Q9J250	Q9j250	pseudomona
7	45	43.7	238	16	Q9CJW5	Q9cjw5	pasteurella
8	45	43.7	301	10	Q9ZQW9	Q9zqw9	oryza sativ
9	44	42.7	257	17	Q97UP0	Q97up0	oryza sativ
10	44	42.7	497	3	Q9C106	Q9cl06	emericella
11	44	42.7	497	3	Q9C1Q5	Q9clq5	emericella
12	44	42.7	497	3	Q9C1Q5	Q9clq5	emericella
13	44	42.7	914	4	Q99493	Q99493	homo sapien
14	44	42.7	1260	5	Q9V468	Q9v468	drosophila
15	44	42.7	1312	4	Q99700	Q99700	homo sapien
16	43.5	42.2	124	2	Q9F273	Q9f273	actinobacil

17	43	41.7	366	5	Q964C6	Q964c6 musca domes
18	43	41.7	516	4	Q9P290	Q9P290 homo sapien
19	43	41.7	625	2	Q9R9E7	Q9R9e7 pseudomonas
20	43	41.7	1100	5	Q9VUE7	Q9Vus7 drosophila
21	42	40.8	241	16	Q9PD74	Q9pd74 xylella fas
22	42	40.8	316	16	Q9HYU2	Q9hyu2 pseudomonas
23	42	40.8	333	16	Q9CLF9	Q9clf9 pasteurella
24	42	40.8	353	5	Q9NBJ2	Q9nbj2 drosophila
25	42	40.8	364	10	Q9SMD5	Q9smd5 lycopersico
26	42	40.8	366	5	Q9NBJ3	Q9nbj3 drosophila
27	42	40.8	377	2	Q9ZAN3	Q9zan3 vibrio angu
28	42	40.8	578	5	Q9Y281	Q9y281 plasmodium
29	42	40.8	684	4	Q9HCM6	Q9hcm6 homo sapien
30	42	40.8	733	11	Q9Z2V1	Q9z2v1 mus musculus
31	42	40.8	738	11	Q9LZ55	Q9l255 mus musculus
32	42	40.8	842	2	Q93JF4	Q93jf4 streptomyce
33	42	40.8	955	4	Q9Y2W1	Q9y2w1 homo sapien
34	42	40.8	1743	3	Q9C3Z2	Q9c3z2 cochllobolu
35	42	40.8	1865	4	Q14I85	Q14i85 homo sapien
36	42	40.8	2531	5	Q16004	Q16004 lytechinus
37	41.5	40.3	94	5	Q9I684	Q9i684 drosophila
38	41.5	40.3	134	4	Q96NR2	Q96nr2 homo sapien
39	41	39.8	115	5	Q23174	Q23174 caenorhabdi
40	41	39.8	205	16	Q9A5D9	Q9a5d9 caulobacter
41	41	39.8	254	16	Q9PHE8	Q9phe8 xylella fas
42	41	39.8	284	5	Q9GTX5	Q9gtx5 plasmodium
43	41	39.8	278	3	Q96RT5	Q96rt5 alternaria
44	41	39.8	280	5	Q27243	Q27243 plasmodium
45	41	39.8	280	5	Q25852	Q25852 plasmodium

## ALIGNMENTS

RESULT	1	
Q9AES0	PRELIMINARY;	PRT: 238 AA.
Q9AES0		
AC	Q9AES0;	
DT	01-JUN-2001 (TrEMBLrel. 17, Created)	
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)	
DT	01-OCT-2001 (TrEMBLrel. 18, Last annotation update)	
DE	RIBONUCLEASE PH-LIKE PROTEIN.	
OS	Pasteurella haemolytica.	
OC	Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;	
OC	Mannheimia.	
OX	NCBI_TaxID=75985;	
OX	NCBI_TaxID=75985;	
RN	[1]	
RN	SEQUENCE FROM N.A.	
RA	Lo R.Y., Graham M.R.;	
RT	"Putative TonB dependent receptor of Mannheimia haemolytica."	
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.	
DR	EMBL: AY028475; AA:29744.1; -	
DR	InterPro: IPR001247; 3_ExoRNase.	
DR	InterPro: IPR002381; RNase_PH.	
DR	Pfam: PF01138; RNase_PH.1.	
DR	PROSITE: PS01277; RIBONUCLEASE_PH.1.	
DR	SEQUENCE 238 AA; 25893 MW; EF0BE4392716BD2F CR064;	

RESULT 2  
O50532  
ID O50532 PRELIMINARY; PRT; 393 AA.  
AC O50532;  
DT 01-JUN-1998 (TREMBLrel. 06, Created)



DR PROSITE; PS01277; RIBONUCLEASE\_PH; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 257 AA; 27726 MW; 522733A6FAD8991A CRC64;

Query Match 44.7%; Score 46; DB 16; Length 257;  
 Best Local Similarity 53.3%; Pred. No. 7.4;  
 Matches 8; Conservative 3; Mismatches 0; Gaps 0;  
 Indels 4; Indels 0; Gaps 0;  
 Db 82 YGMLPRATHSRTRRE 96  
 ||||:||||:  
 2 YGSLPQKSHGRTQDE 16  
 ||||:||||:

RESULT 6  
 Q91250 PRELIMINARY; PRT; 632 AA.

AC Q91250;  
 DT 01-MAR-2001 (TRENBLrel. 16, Created)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
 DE COPPER RESISTANCE PROTEIN A PRECURSOR.  
 GN PCOA OR PA2065.  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 OC Pseudomonas.  
 OX NCBI\_TaxID=287;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN-ATCC 15692 / PA01;  
 RX MEDLINE=20437373; PubMed=10984043;  
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Miziochuchi S.D., Warren P.,  
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
 RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,  
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;  
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an  
 RT opportunistic pathogen.";  
 RL Nature 406:959-964(2000).  
 DR EMBL; AE004633; AAG05453.1; -  
 DR InterPro; IPR001117; Cu-oxidase.  
 DR InterPro; IPR001287; Cu\_nit\_rdtase.  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR InterPro; IPR002355; MultiCu\_oxidase2.  
 DR Pfam; PF00394; Cu-oxidase; 3.  
 DR PRINTS; PR00695; CUNO2RDTASE.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; UNKNOWN\_1.  
 DR PROSITE; PS00079; MULTICOPPER\_OXIDASE1; 1.  
 DR PROSITE; PS00080; MULTICOPPER\_OXIDASE2; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 632 AA; 69851 MW; 229DA2AE86F5B519 CRC64;

Query Match 44.7%; Score 46; DB 16; Length 632;  
 Best Local Similarity 43.8%; Pred. No. 21;  
 Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 3 GSLPQKSHGRTQDENP 18  
 ||||:||||:  
 Db 451 GAMPQSHPAEDGNDP 466

RESULT 7  
 Q9CJW5 PRELIMINARY; PRT; 238 AA.

AC Q9CJW5;  
 DT 01-JUN-2001 (TRENBLrel. 17, Created)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
 DE RPH.  
 GN RPH OR PM1876.  
 OS Pasteurella multocida.

OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
 OC Pasteurella.  
 OX NCBI\_TaxID=747;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=PM70;  
 RX MEDLINE=21145866; PubMed=11248100;  
 RA May B.J., Zhang O., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;  
 RT "Complete genomic sequence of Pasteurella multocida Pm70.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).  
 DR EMBL; AE006225; AAK03960.1; -  
 DR InterPro; IPR001247; 3-EXORNase.  
 DR InterPro; IPR002381; RNase\_PH.  
 DR Pfam; PF01138; RNase\_PH; 1.  
 DR PROSITE; PS01277; RIBONUCLEASE\_PH; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 238 AA; 25902 MW; A8B62C30D492E178 CRC64;

Query Match 43.7%; Score 45; DB 16; Length 238;  
 Best Local Similarity 53.3%; Pred. No. 10;  
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 YGSLPQKSHGRTQDE 16  
 ||||:||||:  
 Db 63 YGMLPRSTHSMQRE 77

RESULT 8  
 Q9ZQW9 PRELIMINARY; PRT; 301 AA.

AC Q9ZQW9;  
 DT 01-MAY-1999 (TRENBLrel. 10, Created)  
 DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
 DE U2 SNRNP AUXILIARY FACTOR, SMALL SUBUNIT.  
 GN U2AF35B.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzoae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99069463; PubMed=9852132;  
 RA Domon C., Lorkovic Z.J., Valcarcel J., Filipowicz W.;  
 RT "Multiple forms of the U2 small nuclear ribonucleoprotein auxiliary  
 RT factor U2AF subunits expressed in higher plants.";  
 RL J. Biol. Chem. 273:34603-34610(1998).  
 DR EMBL; Y18348; CAA77132.1; -  
 DR InterPro; IPR000504; RRM.  
 DR InterPro; IPR000571; Zf-CCCH.  
 DR Pfam; PF00076; rrm; 1.  
 DR Pfam; PF00642; zf-CCCH; 2.  
 DR SMART; SM00360; RRM; 1.  
 DR SMART; SM00356; ZnP\_C3H1; 2.  
 DR PROSITE; PS0102; RRM; 1.  
 SQ SEQUENCE 301 AA; 34338 MW; F054B79C02FD662D CRC64;

Query Match 43.7%; Score 45; DB 10; Length 301;  
 Best Local Similarity 41.2%; Pred. No. 13;  
 Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 YGSLPQKSHGRTQDENP 18  
 ||||:||||:  
 Db 185 YGGRSRSHGRSPSP 201

RESULT 9  
 Q97UP0 PRELIMINARY; PRT; 257 AA.  
 ID Q97UP0  
 AC Q97UP0;

DT 01-OCT-2001 (Tremblrel. 18, Created)  
 DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)  
 DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)  
 DE HYPOTHETICAL PROTEIN SSO2964.  
 GN SSO2964.  
 OS Sulfolobus solfataricus.  
 OC Archaea: Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.  
 OX NCBI\_TaxID=2287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ATCC 35092 / DSM 1617 / P2;  
 RX MEDLINE=21332296; PubMed=11427726;  
 RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,  
 RA Awey M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,  
 RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,  
 RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,  
 RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,  
 RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,  
 RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;  
 RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).  
 DR EMBL; AE006887; AAK43068.1; -.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 257 AA; 28092 MW; BC3A972C9A576AF8 CRC64;

Query Match 42.7%; Score 44; DB 17; Length 257;  
 Best Local Similarity 44.4%; Pred. No. 16;  
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18  
 ||||| : ||| ||  
 Db 79 HYGSLVELHSDPDHNP 96

## RESULT 10

Q9C1Q6 PRELIMINARY; PRT; 497 AA.  
 AC Q9C1Q6;  
 DT 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE ALDEHYDE DEHYDROGENASE ALDH.  
 GN ALDA.  
 OS Emericella nidulans (Aspergillus nidulans).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eurotiales; Trichocomaceae; Emericella.  
 OX NCBI\_TaxID=5072;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21269214; PubMed=11102439;  
 RA Filippi M., Mathieu M., Cirpus I., Panozzo C., Felenbok B.;  
 RT "Regulation of the aldehyde dehydrogenase gene (aldA) and its role in  
 the control of the co-inducer level necessary for induction of the  
 ethanol utilization pathway in Aspergillus nidulans.";  
 RL J. Biol. Chem. 276:6950-6958(2001).  
 DR EMBL; AF260123; AAK18072.1; -.  
 DR HSSP; P05091; 1CW3.  
 DR InterPro; IPR002086; Aldehyde\_dehydr.  
 DR Pfam; PF00171; aldedh; 1.  
 DR PROSITE; PS00070; ALDEHYDE\_DEHYDR\_CYS; 1.  
 FT VARIANT 191 191 E -> Q.  
 FT VARIANT 208 208 G -> P.  
 FT VARIANT 247 247 R -> P.  
 FT VARIANT 409 409 E -> V.  
 SQ SEQUENCE 497 AA; 54138 MW; 9C6CFC62731A25BD CRC64;

Query Match 42.7%; Score 44; DB 3; Length 497;  
 Best Local Similarity 44.4%; Pred. No. 36;  
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18  
 :| | | | | | | |  
 Db 127 YYAGWADKIHGTIDTNP 144

## RESULT 11

Q9C1Q5 PRELIMINARY; PRT; 497 AA.  
 AC Q9C1Q5;  
 DT 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE ALDEHYDE DEHYDROGENASE ALDH15.  
 GN ALDA.  
 OS Emericella nidulans (Aspergillus nidulans).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eurotiales; Trichocomaceae; Emericella.  
 OX NCBI\_TaxID=5072;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21269214; PubMed=11102439;  
 RA Filippi M., Mathieu M., Cirpus I., Panozzo C., Felenbok B.;  
 RT "Regulation of the aldehyde dehydrogenase gene (aldA) and its role in  
 the control of the co-inducer level necessary for induction of the  
 ethanol utilization pathway in Aspergillus nidulans.";  
 RL J. Biol. Chem. 276:6950-6958(2001).  
 DR EMBL; AF260124; AAK18073.1; -.  
 DR HSSP; P05091; 1CW3.  
 DR InterPro; IPR002086; Aldehyde\_dehydr.  
 DR Pfam; PF00171; aldedh; 1.  
 DR PROSITE; PS00070; ALDEHYDE\_DEHYDR\_CYS; 1.  
 DR PROSITE; PS00687; ALDEHYDE\_DEHYDR\_GLU; 1.  
 FT VARIANT 286 286 V -> A.  
 SQ SEQUENCE 497 AA; 54166 MW; 65849D1DCA94A3F5 CRC64;

Query Match 42.7%; Score 44; DB 3; Length 497;  
 Best Local Similarity 44.4%; Pred. No. 36;  
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18  
 :| | | | | | | |  
 Db 127 YYAGWADKIHGTIDTNP 144

## RESULT 12

Q9C1Q4 PRELIMINARY; PRT; 497 AA.  
 AC Q9C1Q4;  
 DT 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE ALDEHYDE DEHYDROGENASE ALDH57.  
 GN ALDA.  
 OS Emericella nidulans (Aspergillus nidulans).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eurotiales; Trichocomaceae; Emericella.  
 OX NCBI\_TaxID=5072;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21269214; PubMed=11102439;  
 RA Filippi M., Mathieu M., Cirpus I., Panozzo C., Felenbok B.;  
 RT "Regulation of the aldehyde dehydrogenase gene (aldA) and its role in  
 the control of the co-inducer level necessary for induction of the  
 ethanol utilization pathway in Aspergillus nidulans.";  
 RL J. Biol. Chem. 276:6950-6958(2001).  
 DR EMBL; AF260125; AAK18074.1; -.  
 DR HSSP; P05091; 1CW3.  
 DR InterPro; IPR002086; Aldehyde\_dehydr.  
 DR Pfam; PF00171; aldedh; 1.  
 DR PROSITE; PS00070; ALDEHYDE\_DEHYDR\_CYS; 1.  
 DR PROSITE; PS00687; ALDEHYDE\_DEHYDR\_GLU; 1.  
 FT VARIANT 338 338 S -> G.



SQ SEQUENCE 497 AA; 54168 MW; 54F425A3B3063875 CRC64;

Query Match 42.7%; Score 44; DB 3; Length 497;  
Best Local Similarity 44.4%; Pred. No. 36;

Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18

Db 127 YYAGWADKIHGQTIDNP 144

RESULT 13

Q99493 ID Q99493 PRELIMINARY; PRT; 914 AA.

DT 01-MAY-1997 (TRENBLrel. 03, Created)

DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)

DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)

DE SCA2 PROTEIN (FRAGMENT).

GN SCA2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OC NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97051922; PubMed=8896557;

RA Imbert G., Saudou F., Ivert G., Devys D., Trottier Y., Garnier J.M.,

RA Weber C., Mandel J.L., Cancel G., Abbas N., Duerr A., Didierjean O.,

RA Stevanin G., Agid Y., Brice A.;

RT "Cloning of the gene for spinocerebellar ataxia 2 reveals a locus with

RT high sensitivity to expanded CAG/glutamine repeats.";

RL Nat. Genet. 14:285-291(1996).

DR EMBL: Y08262; CAA69589.1; -;

FT NON\_TER 1

SQ SEQUENCE 914 AA; 97862 MW; A173ED4B3F36DE53 CRC64;

Query Match 42.7%; Score 44; DB 3; Length 914;

Best Local Similarity 50.0%; Pred. No. 73;

Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 3 GSLPQKSHGRTQDENP 18

Db 441 GMSFSRSTSHTSDFNP 456

RESULT 14

Q9V468 ID Q9V468 PRELIMINARY; PRT; 1260 AA.

AC Q9V468;

DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)

DE BCDA:ID19168 OR CG9776.

GN BCDA:ID19168 OR CG9776.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OC NCBI\_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Cocayne J.D.,

RA Adamatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brannon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,  
RA Foster G., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

RN [2]

RP SEQUENCE FROM N.A.

RA Tsang G., Brokstein P., Frise E., Harvey D., Evans-Holm M.,

RA Lewis S.E., Sun C., Rubin G.M.;

RT "Full Length Drosophila melanogaster cDNA sequence.";

RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AE003606; AAF52146.1; -;

DR EMBL: AF160940; AAD46880.1; -;

DR FlyBase: FBgn0027866; BCDA:ID19168.

DR InterPro: IPR000822; Znf-C2H2

DR PROSITE: PS00028; ZINC\_FINGER\_C2H2\_1; UNKNOWN\_1.

SQ SEQUENCE 1260 AA; 140294 MW; 098296D9FEA695CA CRC64;

Query Match 42.7%; Score 44; DB 5; Length 1260;

Best Local Similarity 80.0%; Pred. No. 11e+02;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 QKSHGRTQDE 16

Db 382 QKSHGRTQDE 391

RESULT 15

Q99700 ID Q99700 PRELIMINARY; PRT; 1312 AA.

AC Q99700;

DT 01-MAY-1997 (TRENBLrel. 03, Created)

DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)

DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)

DE ATAXIN-2.

GN SCA2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OC NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97051920; PubMed=8896555;

RA Pulst S.-M., Nechiporuk A., Nechiporuk T., Gispert S., Chen X.-N.,

RA Lopes-Cendes I., Pearlman S., Starkman S., Orozco-Diaz G., Lunkes A.,

RA DeJong P., Rouleau G.A., Auburger G., Korenberg J.R., Figueroa C.,

RA Sahba S.;  
RT "Moderate expansion of a normally biallelic trinucleotide repeat in  
RL spinocerebellar ataxia type 2.";  
RL Nat. Genet. 14:269-276(1996).  
DR EMBL; U70323; AAB19200.1; .  
SQ SEQUENCE 1312 AA; 140140 MW; CF6E358C14A83AF5 CRC64;

Query Match 42.7%; Score 44; DB 4; Length 1312;  
Best Local Similarity 50.0%; Pred. No. 1.1e+02;  
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 3 GSLPQKSHGRTQDENP 18  
||:|:| | | | |  
Db 521 GSMPSRSTSHTSDENP 536

Search completed: August 28, 2002, 16:41:25  
Job time: 377 sec